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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF EXPRESS MAILING
Hereby certify that this paper and the documents and/or fees referred to as attached therein are being deposited with the United States Postal Service on November 21, 2000 in an envelope as "Express Mail Post Office to Addressee" service under 37 CFR §1.10, Mailing Label Number **EL711139035US**, addressed to the Assistant Commissioner for Patents, Washington, DC 20231.

Torrance Straiten

Torrance Straiten

Attorney Docket No.: CYTOP007C2

First Named Inventor: Vaisberg et al.

UTILITY PATENT APPLICATION TRANSMITTAL (37 CFR. § 1.53(b))

(Continuation, Divisional or Continuation-in-part application)

Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

Sir: This is a request for filing a patent application under 37 CFR. § 1.53(b) in the name of inventors: **Eugeni A. Vaisberg, Cynthia L. Adams, James H. Sabry, Anne M. Crompton**

For: **DATABASE SYSTEM INCLUDING COMPUTER FOR PREDICTIVE CELLULAR BIOINFORMATICS**

This application is a ☒ Continuation ☐ Divisional ☐ Continuation-in-part

of prior Application No.: 09/311,996, from which priority under 35 U.S.C. §120 is claimed.

Application Elements:

- ☒ 53 Pages of Specification, Claims and Abstract
- ☒ 24 Sheets of informal Drawings
- ☒ Declaration and Power of Attorney
  - ☐ Newly executed
  - ☒ Copy from a prior application (37 CFR 1.63(d) for a continuation or divisional). The entire disclosure of the prior application from which a copy of the declaration is herein supplied is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
    - ☐ Deletion of inventors Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

Accompanying Application Parts:

- ☐ Assignment and Assignment Recordation Cover Sheet (recording fee of $40.00 enclosed)

☐ Power of Attorney
☐ 37 CFR 3.73(b) Statement by Assignee
☒ Information Disclosure Statement with Form PTO-1449 ☐ Copies of IDS Citations
☐ Preliminary Amendment (*New claims numbered after highest original claim in prior application.*)
☒ Return Receipt Postcard
☒ Other: Appendix A
☒ Other: Associate Power of Attorney and Change of Correspondence Address in Application

Claim For Foreign Priority

☐ Priority of Application No. filed on
is claimed under 35 U.S.C. § 119.
☐ The certified copy has been filed in prior application U.S. Application No.
☐ The certified copy will follow.

SCANNED, # 9

Extension of Time for Prior Pending Application

☐ A Petition for Extension of Time is being concurrently filed in the prior pending application. A copy of the Petition for Extension of Time is attached.

Amendments

☒ Amend the specification by inserting before the first line the sentence: "This is a
☒ Continuation ☐ Continuation-in-part ☐ Divisional
application of co-pending prior
☒ Application No. 09/311,996 filed on May 14. 1999,
☐ International Application filed on which designated the United States,
the disclosure of which is incorporated herein by reference."

☐ Cancel in this application original claims of the prior application before calculating the filing fee. (*At least one original independent claim must be retained.*)

Fee Calculation (37 CFR § 1.16)

☒ Applicant is entitled to Small Entity Status under 37 C.F.R. §1.27.

	(Col. 1) Total Claims		(Col. 2) Claims	(Col. 3) Present Extra	Rate	Additional Fee
TOTAL	48	MINUS	20	= 28	x 18	504.00
INDEP.	4	MINUS	3	= 1	x 80	80.00
[ ] First presentation of multiple dependent claim					$270	
Basic Filing Fee under 37 C.F.R. §1.16(a)					$710	710.00
TOTAL						1294.00
SMALL ENTITY 50% FILING FEE REDUCTION (if applicable)						647.00

☒ Check No. in the amount of $647.00 is enclosed.
☒ The Commissioner is authorized to charge any fees beyond the amount enclosed which may be required, or to credit any overpayment, to Deposit Account No. 500388 (Order No. CYTOP007C2).

SCANNED, # 9

General Authorization for Petition for Extension of Time (37 CFR §1.136)

☒ Applicants hereby make and generally authorize any Petitions for Extensions of Time as may be needed for any subsequent filings. The Commissioner is also authorized to charge any extension fees under 37 CFR §1.17 as may be needed to Deposit Account No. 500388 (Order No. CYTOP007C2).

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22434
PATENT TRADEMARK OFFICE

Date: 11/21/00

Jeffrey K. Weaver
Registration No. 31,314

Attorney Docket No.: 019681-000400US

PATENT APPLICATION

A DATABASE SYSTEM INCLUDING COMPUTER CODE FOR PREDICTIVE CELLULAR BIOINFORMATICS

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A DATABASE SYSTEM INCLUDING COMPUTER CODE FOR PREDICTIVE CELLULAR BIOINFORMATICS

CROSS-REFERENCES TO RELATED APPLICATIONS

The following commonly-owned co-pending applications, including this one, are being filed concurrently and the others are hereby incorporated by reference in their entirety for all purposes:

1. U.S. Patent Application Serial No. _____________, James H. Sabry, et al., titled, "A DATABASE METHOD FOR PREDICTIVE CELLULAR BIOINFORMATICS," (Attorney Docket Number 19681-000100US);

2. U.S. Patent Application Serial No. _____________, James H. Sabry, et al., titled, "A DATABASE SYSTEM FOR PREDICTIVE CELLULAR BIOINFORMATICS," (Attorney Docket Number 19681-000200US);

3. U.S. Patent Application Serial No. _____________, Cynthia L. Adams, et. al., titled, "A DATABASE SYSTEM AND USER INTERFACE FOR PREDICTIVE CELLULAR BIOINFORMATICS," (Attorney Docket Number 19681-000300US); and

4. U.S. Patent Application Serial No. _____________, Eugeni A. Vaisberg, et al., titled, "A DATABASE SYSTEM INCLUDING COMPUTER CODE FOR PREDICTIVE CELLULAR BIOINFORMATICS," (Attorney Docket Number 19681-000400US)

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BACKGROUND OF THE INVENTION

The present invention provides information technology based techniques including computer software in therapeutics or drug discovery. In an exemplary embodiment, the present invention provides software for determining information about properties of substances based upon information about structures of living, fixed or non-

living cells, or cell fractions. Computer code according to the present invention enable researchers and scientists to identify promising candidates in the search for new and better medicines and medical techniques.

For a long time, researchers in the pharmaceutical field have sought for better ways of searching for substances possessing properties which make them suitable as medicines. In the early days, researches generally relied upon dyes, or extracts from plants, , or microbiological broths for such substances. Examples of such substances include aspirin, and antibiotics.

Substances having desirable bio-active properties, however, are often difficult to isolate and identify. Advances in organic chemistry such as rapid chemical synthesis techniques have increased the number of compounds that researchers want to test for biological activity. Conventionally, substances were often tested on humans or animal subjects to determine biological activity. While results from such tests can be highly predictive, these types of tests can be time consuming, limiting the progress of the testing.

There have been some attempts to use image acquisition techniques to screen for large numbers of molecules based upon cell information. Conventional image acquisition systems exist that generally capture digitized images of discrete cells for identification purposes. Identification often occurs during the image capturing step, which is limiting. In most cases, these conventional techniques cannot comprehensively provide for complete cellular information but can only be used to identify a fairly limited set of information.

What is needed are techniques for collecting and managing information useful in finding the effects of manipulations on cell function, response or behavior.

SUMMARY OF THE INVENTION

According to the present invention, techniques for using information technology in therapeutics or drug discovery. In an exemplary embodiment, computer software for determining information about the properties of substances based upon information about a structure or the morphology of living, fixed or dead cells (e.g., elements, cell portions and cell fractions) exposed to substances are provided. Computer software according to the present invention enables researchers and/or scientists to

identify promising candidates in the search for new and better medicines or treatments using, for example, a cellular informatics database.

According to the present invention, a computer program for identification and verification of biological properties of substances can include code that administers a sample of the substance to a cell. The code determines one or more features for two or more cell components, or markers, in the presence of the substance. The code can form one or more descriptors from the features. Descriptors can be formed by combining features of two or more cell components as identified using the markers. The code can then search one or more descriptors obtained from prior administered substances upon cells in order to locate descriptors having a relationship to the descriptors noted for the substance under study. The code predicts properties of the administered substance based upon the properties of the prior administered substances using the relationship between the descriptors. The code can provide for identifying properties of substances based upon effects on cell characteristics. Candidate drug mechanisms of action, potency, specificity, pharmacodynamic, and pharmacokinetic parameters, toxicity, and the like can be used as substance properties.

In another embodiment according to the present invention, computer programs for animal model selection, clinical trial design and patient management can be provided.

In a further embodiment according to the present invention, techniques for using cellular information in predictive methods for acquiring, analyzing and interpreting cellular data are incorporated into a computer program product including code. In one such embodiment, code for predicting properties of an unknown substance based upon information about effects of one or more known substances on a cell population is provided. The code performs a variety of tasks, such as populating a database with descriptors of cells subjected to known substances. Such descriptors can be determined from imaging the cell population. However, in some embodiments, descriptors can be derived by measurements and combinations of measurements and the like. The code determines descriptors for the unknown substance from imaging a second cell population. The second cell population has been treated with the unknown substance. Then, the code can determine a relationship between the descriptors determined from the unknown substance with the descriptors determined from the known substance. From this relationship, an inference can be made about the unknown substance.

In a yet further embodiment according to the present invention, a computer program for determining properties of a manipulation based upon effects of the manipulation on one or more cell fractions. The computer program includes code that can provide the manipulation to the cell fractions. The code can also determine one or more features of markers corresponding to cell components within the cell fractions in the presence of the manipulation. Code for forming descriptors from the features is also included. Code for searching in a database in order to locate descriptors based upon at least one of the descriptors obtained from the manipulation is also included. The computer program can include code for determining, based upon the descriptors located in the database, properties of the manipulation.

Moreover, the present invention provides computer software for mapping a manipulation of cells based upon a morphological characteristic. The computer software includes code for providing a plurality of cells, e.g., dead, live, cell fragments, cell components, cell substructures. The software also includes code for manipulating the plurality of cells, where manipulation occurs using a source(s) from one or a combination selected from an electrical source, a chemical source, a thermal source, a gravitational source, a nuclear source, a temporal source, and a biological source. The software code captures a morphological value from the plurality of cells. The morphological value can include one or any combination of characteristics such as a cell count, an area, a perimeter, a length, a breadth, a fiber length, a fiber breadth, a shape factor, an elliptical form factor, an inner radius, an outer radius, a mean radius, an equivalent radius, an equivalent sphere volume, an equivalent prolate volume, an equivalent oblate volume, an equivalent sphere surface area, an average gray value, a total gray value, and an optical density. The software code also assigns a degree of presence of the morphological value, and stores the morphological value from the plurality of cells. These values can be used for a statistical analysis to produce a statistical profile.

Still further, the present invention provides a computer program product for populating a database with manipulated biological information, e.g., cellular enzymatic activities, cellular cascades, cellular promoters, transcription factors, translation factors, cell cycle stage and apoptosis. The computer program product includes code for providing a plurality of cells in various stages of the cell cycle, where the stages of the cell cycle may include at least one selected from interphase, G0 phase, G1 phase, S phase, G2 phase, M phase which itself includes prophase, prometaphase, metaphase, anaphase, and telophase. The computer program also includes code for

manipulating each of the cells in the various stages of the cell cycle. The computer program includes code for capturing (e.g., image acquisition) an image of the plurality of manipulated cells where the code for capturing provides a morphometric characteristic of the manipulated cells. The computer program product also includes code for populating a database with the morphometric characteristic of the plurality of manipulated cells. Accordingly, the present invention provides software for populating a database, which can be queried.

Numerous benefits are achieved by way of the present invention over conventional techniques. The present invention can provide techniques for predictive cellular bioinformatics that can stream line a number of important decisions made in the drug discovery industry, medical diagnostics and biological research. The present invention can be implemented on conventional hardware including databases. In other aspects, the present invention can find useful information about substances as well as cells or portions of cells, especially morphology. Embodiments can provide a holistic approach to cell based drug discovery that enables the understanding of properties of substances based on their overall effects on cell biology. The properties include, among others, clinical uses and descriptors, human and veterinary diagnostic uses and tests, or human and veterinary prognostic uses and tests. Depending upon the embodiment, one or more of these advantages may be present. These and other benefits are described throughout the present specification.

A further understanding of the nature and advantages of the invention herein may be realized by reference to the remaining portions of the specification and the attached drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates a block diagram of a system according to an embodiment according to the present invention;

Figs. 2A-2K illustrate representative block diagrams of simplified process steps in a particular embodiment according to the present invention;

Fig. 3A-3F illustrate representative quantified descriptors of effects of manipulations on images of cells in a particular experiment;

Fig. 4 illustrates example images for different types of morphologies in a particular experiment;

Fig. 5 illustrates a distribution of various morphologies in a cell population responsive to drug concentration in a particular experiment;

Fig. 6 illustrates a graph of quantified descriptors of effects of manipulations on cell cytoarchitecture in a particular experiment;

Fig. 7 illustrates effects of external agents on cell cytoarchitecture in a particular experiment;

Fig. 8 illustrates 4 panels, one for each marker for a plurality of A549 cells in a particular experiment;

Fig. 9 illustrates 4 panels, one for each marker for a plurality of OVCAR-3 cells in a particular experiment;

Fig. 10 illustrates 4 panels for each marker for a plurality of OVCAR-3 cells at 20x in a particular experiment;

Fig. 11 illustrates 4 panels for each marker for a plurality of OVCAR-3 cells at 40x in a particular experiment;

Fig. 12 illustrates a representative input for a morphometric analysis program in a particular embodiment according to the present invention; and

Figs. 13-14 illustrate examples of the generation of pseudo-sequences and clustering in a particular embodiment according to the present invention.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

According to the present invention, techniques for using information technology in therapeutics or drug discovery. In an exemplary embodiment, techniques for determining information about the properties of substances based upon information about the structure of living, fixed or non-living cells exposed to the substances are provided. Computer software according to the present invention enables researchers and/or scientists to identify promising candidates in the search for new and better medicines or treatments using, for example, a cellular informatics database. An embodiment according to the present invention is marketed under the name Cytometrix™, which is not intended to be limiting.

In a particular embodiment according to the present invention, a cellular informatics database is provided. Embodiments according to the present invention can provide techniques for predicting candidate drug mechanisms of action, potency, specificity, structure, toxicity and the like. In some embodiments, substances or other manipulations can be used for target identification and validation. Embodiments can be

useful in areas such as animal model selection, clinical trial design and patient management, including prognostics, drug response prediction and adverse effect prediction.

Fig. 1 depicts a block diagram of a host computer system 110 suitable for implementing the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Host computer system 110 includes a bus 112 which interconnects major subsystems such as a central processor 114, a system memory 116 (typically RAM), an input/output (I/O) controller 118, an external device such as a display screen 124 via a display adapter 126, a keyboard 132 and a mouse 146 via an I/O controller 118, a SCSI host adapter (not shown), and a floppy disk drive 136 operative to receive a floppy disk 138. Storage Interface 134 may act as a storage interface to a fixed disk drive 144 or a CD-ROM player 140 operative to receive a CD-ROM 142. Fixed disk 144 may be a part of host computer system 110 or may be separate and accessed through other interface systems.

The system has other features. A network interface 148 may provide a direct connection to a remote server via a telephone link or to the Internet. Network interface 148 may also connect to a local area network (LAN) or other network interconnecting many computer systems. Many other devices or subsystems (not shown) may be connected in a similar manner. Also, it is not necessary for all of the devices shown in Fig. 1 to be present to practice the present invention, as discussed below. The devices and subsystems may be interconnected in different ways from that shown in Fig. 1. The operation of a computer system such as that shown in Fig. 1 is readily known in the art and is not discussed in detail in this application. Code to implement the present invention, may be operably disposed or stored in computer-readable storage media such as system memory 116, fixed disk 144, CD-ROM 140, or floppy disk 138.

Although the above has been described generally in terms of specific hardware, it would be readily apparent to one of ordinary skill in the art that many system types, configurations, and combinations of the above devices are suitable for use in light of the present disclosure. Of course, the types of system elements used depend highly upon the application. Other examples of system can be found in co-pending application U.S. Application No. ____________ (Attorney Docket No. 19681-000200), which has been noted above.

Fig. 2A illustrates a representative block flow diagram of simplified process steps of a method for determining properties of a manipulation based upon effects of the manipulation on one or more portions of one or more cells in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. In a step 200, one or more samples of cells can be provided. These cells can be live, dead, or cell fractions. The cells also can be in one of many cell cycle stages, including G0, G1, S, G2 or M phase, which itself includes the following mitotic stages: prophase, prometaphase, metaphase, anaphase, and telophase. Cell components may be tracked using one or more markers. In a presently preferable embodiment, many useful and novel cell markers can be used.

Cell components tracked in presently preferable embodiments can include proteins, protein modifications, genetically manipulated proteins, exogenous proteins, enzymatic activities, nucleic acids, lipids, carbohydrates, organic and inorganic ion concentrations, sub-cellular structures, organelles, plasma membrane, adhesion complex, ion channels, ion pumps, integral membrane proteins, cell surface receptors, G-protein coupled receptors, tyrosine kinase receptors, nuclear membrane receptors, ECM binding complexes, endocytotic machinery, exocytotic machinery, lysosomes, peroxisomes, vacuoles, mitochondria, golgi apparatus, cytoskeletal filament network, endoplasmic reticulum, nuclear membrane, proteosome apparatus, chromatin, nucleolus, cytoplasm, cytoplasmic signaling apparatus, microbe specializations and plant specializations.

The following table illustrates some markers and cell components commonly used by embodiments according to the present invention. Other markers can be used in various embodiments without departing from the scope of the invention.

Cell component	Marker	Disease State
Plasma membrane (including overall cell shape)	Carbocyanine dyes Phosphatidylserine Various lipids Glycoproteins	Apoptosis-Cancer Apoptosis-Neural degenerative Ds
Adhesion complexes	Cadherins Integrins Occludin Gap junction ERM proteins CAMs Catenins Desmosomes	Thrombosis Metastasis Wound healing Inflammatory Ds Dermatologic Ds
Ion Channels and Pumps	Na/K Atpase Calcium channels Serotonin reuptake pump CFTR	Cystic fibrosis Depression Congestive Heart Failure Epilepsy
G coupled receptors	β adrenergic receptor Angiotensin receptor	Hypertension Heart Failure Angina
Tyrosine kinase receptors	PDGF receptor FGF receptor IGF receptor	Cancer Would healing Angiogenesis Cerebrovascular Ds
ECM binding complexes	Dystroglycan Syndecan	Muscular Dystrophy
Endocytotic machinery	Clathrin Adaptor proteins COPs Presenilins Dynamin	Alzheimer's Ds

Exocytotic machinery	SNAREs Vesicles	Epilepsy Tetanus Systemic Inflammation Allergic Reactions
Lysosomes	Acid phosphatase Transferrin	Viral diseases
Peroxisomes/Vacuoles		Neural degenerative Ds
Mitochondria	Caspases Apoptosis inducing factor F1 ATPase Fluorescein Cyclo-oxygenase	Apoptosis Neural degenerative Ds Mitochondrial Cytopathies Inflammatory Ds
Golgi Apparatus	Lens Culinaris DiOC6 carbocyanine dye COPs	
Cytoskeletal Filament Networks	Microtubules Actin Intermediate Filaments Kinesin, dynein, myosin Microtubule associated proteins Actin binding proteins Rac/Rho Keratins	Cancer Neural degenerative Ds Inflammatory Ds Cardiovascular Ds Skin Ds
Endoplasmic Reticulum	SNARE PDI Ribosomes	Neural degenerative Ds
Nuclear Membrane	Lamins Nuclear Pore Complex	Cancer
Proteosome Apparatus	Ubiquityl transferases	Cancer

Chromatin	DNA Histone proteins Histone deacetylases Telomerases	Cancer Aging
Nucleolus	Phase markers	
Cytoplasm	Intermediary Metabolic Enzymes BRCA1	Cancer
Cytoplasmic Signaling Apparatus	Calcium Camp PKC pH	Cardiovascular Ds Migraine Apoptosis Cancer
Microbe Specializations	Flagella Cilia Cell Wall components: Chitin synthase	Infectious Ds
Plant specializations	Choloroplast Cell Wall components	Crop Protection

Then, in a step 202, one or more samples of the manipulation can be provided to one or more of the cells or cell fractions. Manipulations can comprise chemical, biological, mechanical, thermal, electromagnetic, gravitational, nuclear, temporal factors, and the like. For example, manipulations could include exposure to chemical compounds, including compounds of known biological activity such as therapeutics or drugs, or also compounds of unknown biological activity. Or exposure to biologics that may or may not be used as drugs such as hormones, growth factors, antibodies, or extracellular matrix components. Or exposure to biologics such as infective materials such as viruses that may be naturally occurring viruses or viruses engineered to express exogenous genes at various levels. Bioengineered viruses are one example of manipulations via gene transfer. Other means of gene transfer are well known in the art and include but are not limited to electroporation, calcium phosphate precipitation, and lipid-based transfection. Manipulations could also include delivery of

antisense polynucleotides by similar means as gene transfection. Other genetic manipulations include gene knock-outs gene over-expression or gene mutations. Manipulations also could include cell fusion. Physical manipulations could include exposing cells to shear stress under different rates of fluid flow, exposure of cells to different temperatures, exposure of cells to vacuum or positive pressure, or exposure of cells to sonication. Manipulations could also include applying centrifugal force. Manipulations could also include changes in gravitational force, including sub-gravitation. Manipulations could include application of a constant or pulsed electrical current. Manipulations could also include irradiation. Manipulations could also include photobleaching which in some embodiments may include prior addition of a substance that would specifically mark areas to be photobleached by subsequent light exposure. In addition, these types of manipulations may be varied as to time of exposure, or cells could be subjected to multiple manipulations in various combinations and orders of addition. Of course, the type of manipulation used depends upon the application.

Then, in a step 204, one or more descriptors of a state in the portions of the cells in the presence of the manipulation can be determined based upon the images collected by the imaging system. Descriptors can comprise scalar or vector values, representing quantities such as area, perimeter, dimensions, intensity, aspect ratios, and the like. Other types of descriptors include one or any combination of characteristics such as a cell count, an area, a perimeter, a length, a breadth, a fiber length, a fiber breadth, a shape factor, an elliptical form factor, an inner radius, an outer radius, a mean radius, an equivalent radius, an equivalent sphere volume, an equivalent prolate volume, an equivalent oblate volume, an equivalent sphere surface area, an average intensity, a total intensity and an optical density. In some embodiments, descriptors can include averages or standard deviation values, or frequency statistics from other descriptors collected across a population of cells. In some embodiments, descriptors can be reduced using techniques such as principal component analysis and the like. A presently preferable embodiment uses descriptors selected from the following table. Other descriptors can also be used without departing from the scope of the invention.

Name of Parameter	Explanation/Comments
Count	Number of objects
Area	
Perimeter	
Length	X axis
Width	Y axis
Shape Factor	Measure of roundness of an object
Height	Z axis
Radius	
Distribution of Brightness	
Radius of Dispersion	Measure of how dispersed the marker is from its centroid
Centroid location	x-y position of center of mass
Number of holes in closed objects	Derivatives of this measurement might include, for example, Euler number (= number of objects - number of holes)
Elliptical Fourier Analysis (EFA)	Multiple frequencies that describe the shape of a closed object
Wavelet Analysis	As in EFA, but using wavelet transform
Interobject Orientation	Polar Coordinate analysis of relative location
Distribution Interobject Distances	Including statistical characteristics
Spectral Output	Measures the wavelength spectrum of the reporter dye. Includes FRET
Optical density	Absorbance of light
Phase density	Phase shifting of light
Reflection interference	Measure of the distance of the cell membrane from the surface of the substrate
1,2 and 3 dimensional Fourier Analysis	Spatial frequency analysis of non closed objects
1,2 and 3 dimensional Wavelet Analysis	Spatial frequency analysis of non closed objects
Eccentricity	The eccentricity of the ellipse that has the same second moments as the region.

	A measure of object elongation.
Long axis/Short Axis Length	Another measure of object elongation.
Convex perimeter	Perimeter of the smallest convex polygon surrounding an object
Convex area	Area of the smallest convex polygon surrounding an object
Solidity	Ratio of polygon bounding box area to object area.
Extent	proportion of pixels in the bounding box that are also in the region
Granularity	
Pattern matching	Significance of similarity to reference pattern
Volume measurements	As above, but adding a z axis

Then, in a step 205, a database of cell information can be provided. Next, in a step 206, a plurality of descriptors can be searched from a database of cell information in order to locate descriptors based upon one of the descriptors of the manipulation. Then, in a step 208, properties of the manipulation are determined based upon the properties of the located descriptors. Properties can comprise toxicity, specificity against a subset of tumors, mechanisms of chemical activity, mechanisms of biological activity, structure, adverse biological effects, biological pathways, clinical effects, cellular availability, pharmacological availability, pharmacodynamic properties, clinical uses and descriptors, pharmacological properties, such as absorption, excretion, distribution, metabolism and the like.

In a particular embodiment, step 206 comprises determining matching descriptors in the database corresponding to a prior administration of the manipulation to the descriptors of the present administration of the manipulation. In a particular embodiment according to the present invention, measurements of scalar values can provide predictive information. A database can be provided having one or more "cellular fingerprints" comprised of descriptors of cell-substance interactions of drugs having known mechanisms of action with cells. Such fingerprints can be analyzed, classified and/or compared using a plurality of techniques, such as statistical classification and clustering, heuristic classification techniques, a technique of creating "phylogenetic trees" based on various distance measures between cellular fingerprints from various drugs. In a

present embodiment, scalar, numeric values can be converted into a nucleotide or amino acid letter. Once converted into a corresponding nucleotide representation, the fingerprints can be analyzed and compared using software and algorithms known in the art for genetic and peptide sequence comparisons, such as GCG, a product of Genetics Computer Group, with company headquarters in Madison WI. In an alternative embodiment, numeric values for the fingerprints can be used by comparison techniques. A phylogenetic tree can be created that illustrates a statistical significance of the similarity between fingerprints for the drugs in the database. Because the drugs used to build the initial database are of known mechanism, it can be determined whether a particular scalar value in a fingerprint is statistically predictive. Finally, a compound fingerprint with no known mechanism of action can be queried against the database and be statistically compared and classified among the drugs in the database that the compound most resembles.

In a particular embodiment, relationships between measured morphological properties of images and physiological conditions can be determined. Relationships can include, for example, treatment of different cell lines with chemical compounds, or comparing cells from a patient with control cells, and the like. In a presently preferable embodiment, a clustering can be performed on acquired image feature vectors. Some embodiments can comprise statistical and neural network - based approaches to perform clustering and fingerprinting of various features. The foregoing is provided as merely an example, and is not intended to limit the scope of the present invention. Other techniques can be included for different types of data.

In some embodiments, clustering and fingerprinting can be performed on features extracted from cell images. In a presently preferable embodiment, procedures for comparisons and phylogenetic analysis of biological sequences can be applied to data obtained from imaging cells.

Select embodiments comprising such approaches enable the use of a broad array of sophisticated algorithms to compare, analyze, and cluster gene and protein sequences. Many programs performing this task are known to those of ordinary skill in the art, such as for example, http://evolution.genetics.washington.edu/phylip.html, and http://evolution.genetics.washington.edu/phylip/software.html.

Embodiments can perform such analysis based upon factors such as numerical value, statistical properties, relationships with other values, and the like. In a particular embodiment, numbers in a numerical features vector can be substituted by one

or more of nucleic acid or amino acid codes. Resulting "pseudo-sequences" can be subjected to analysis by a sequence comparison and clustering program. Depending upon the application, many different ways of using the database can be provided. Further details of a step of manipulation are noted more particular below.

Fig. 2B illustrates a representative block flow diagram of simplified process steps for determining one or more descriptors of a state in the portions of the cells in the presence of the manipulation of step 204 of Fig. 2A in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. In a step 212, a picture of a target is obtained. A target can be one or more cells, or portions of cells in select embodiments according to the invention. Then, in a step 214, a digitized representation of the picture obtained in step 212 is determined. In some embodiments, steps 214 and step 212 can comprise a single step. These embodiments use a digital imaging means such as a digital camera, to obtain a digital image of the target directly. Next, in a step 216, the digital representation of the image is processed to obtain image features. Image features can include such quantities as area, perimeter, dimensions, intensity, gray level, aspect ratios, and the like. Then, in a step 218 descriptors can be determined from the image features. Descriptors can comprise scalar or vector quantities and can comprise the image descriptors themselves, as well as derived quantities, such as shape factor derived by a relationship 4π * area / perimeter, and the like.

In a preferred embodiment, cells can be placed onto a microscope, such as a Zeiss microscope, or its equivalent as known in the art. A starting point, named Site A1, is identified to the microscope. A plurality of exposure parameters can be optimized for automated image collection and analysis. The microscope can automatically move to a new well, automatically focus, collect one or more images, move to a next well, and repeat this process for designated wells in a multiple well plate. A file having a size and an intensity distribution measurement for each color and rank for each well can then be created for the images acquired. Based on this information, a user or a computer can revisit sites of interest to collect more data, if desired, or to verify automated analysis. In a presently preferred embodiment, image automatic focus and acquisition can be done using computer software controlling the internal Z-motor of the microscope. Images are taken using a 10x, 20x, or 40x air long working distance objectives. Sometimes multiple

images are collected per well. Image exposure times can be optimized for each fluorescent marker and cell line. The same exposure time can be used for each cell line and fluorescent marker to acquire data.

Fig. 2C illustrates a representative block flow diagram of simplified process steps for obtaining images of cell components of step 212 of Fig. 2B in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2C illustrates a step 220, of providing a sample to the imaging device. Samples can be provided in 96 well plates and the like. The sample may be loaded into a microscope, such as a Zeiss microscope or equivalent. In a step 222, a light is used to illuminate the first sample, which may be contained in a first well designated A1. Then, in a step 224, an automatic focusing procedure is performed for the site. In a particular embodiment, the plate holding the samples is moved to perform automatic focusing of the microscope. In an alternative embodiments, focusing can be performed by moving optical components of the microscope and the like. In a step 226, images are collected for the site. Images can be collected for every color at every site. Present embodiments can provide images for up to four colors. However, embodiments are contemplated that can provide more colors by using either a monochromator or by digitally separating overlapping fluorophores. Cell growth and density information is collected. In some embodiments, imaging can be facilitated using one or more biosensors, molecules such as non-proteins, i.e., lipids and the like, that are luminescently tagged. However, some embodiments can also use fluorescence polarization and the like. Further, embodiments can detect differences in spectral shifts of luminescent markers. In a step 228, a determination is made whether more images need to be taken for a particular color. If this is so, then processing continues at step 226 with a different color. Otherwise, processing continues with a decisional step 230. Images can now be taken by repeating step 226. In a step 230, a determination is made whether more images need to be taken in order to obtain images for all fields of view for the sample. If this is so, then in a step 232 a field of view is determined and the sample is moved to this new field of view. Images for the new field of view can now be taken by repeating step 226. Then, in a decisional step 234, after images for fields of view in a sample have been obtained, a determination is made whether any further samples remain to be analyzed. If so, a new sample is brought into view and processing continues with step 220. Otherwise, image processing is complete

and data analysis is performed on the images. In a presently preferable embodiment, image data can be stored on a CD ROM using a CD ROM burner, removable storage units, such as ZIP drives made by IOMEGA, and the like. However, other mass storage media can also be used.

Fig. 2D illustrates a representative block flow diagram of simplified process steps for processing digitized representations of step 216 of Fig. 2B in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2D illustrates a step 240, of thresholding a digitized image input. Thresholding provides a specific intensity level, such that pixels darker than the threshold are deemed black, and pixels lighter than the threshold are considered white. The resulting image can be processed using binary image processing techniques in order to extract regions. Then, in a step 242, the digitized image input is subjected to edge detection. Edge detection can be accomplished by means of passing a Sobol operator over the entire image and computing new pixel values based upon the contents of the Sobol operator and the original image. However, embodiments can also use other techniques, such as Fast Fourier Transforms (FFT) and the like as known in the art without departing from the scope of the present invention. Then, in a step 244, the regions and objects determined by step 240 and step 242 can be determined based upon image processing techniques.

In a step 246, the regions and objects determined by step 244 can be processed in view of a plurality of classification heuristics to determine cell state based upon selectable criteria. Further, in some embodiments, morphological criteria can be used based upon a cell type to determine cell state. Next, in a step 248, a plurality of region features can be determined. For example, in a representative embodiment, image features can include such quantities as area, perimeter, dimensions, intensity, gray level, aspect ratios, and the like.

In a particular embodiment according to the present invention, data analysis techniques for describing the fluorescence patterns of markers in multiple cell lines in the presence and absence of compounds are provided. Automated image analysis techniques can include determining one or more regions from around nuclei, individual cells, organelles, and the like, called "objects" using a thresholding function. Objects that reside on the edge of an image can be included or excluded in various embodiments. An average population information about an object can be determined and recorded into a

database, which can comprise an Excel spreadsheet, for example. However, embodiments can use any recording means without departing from the scope of the present invention. Values measured can be compared to the visual image. One or more types of numerical descriptors can be generated from the values. For example, descriptors such as a Number of objects, an Average, a standard deviation of objects, a Histogram (number or percentage of objects per bin, average, standard deviation), and the like can be determined.

In a particular embodiment according to the present invention, data can be analyzed using morphometric values derived from any of a plurality of techniques commonly known in the art. Fluorescent images can be described by numerical values, such as for example, an area, a fluorescence intensity, a population count, a radial dispersion, a perimeter, a length, and the like. Further, other values can be derived from such measurements. For example, a shape factor can be derived according to a relationship 4π * area / perimeter. Other values can be used in various embodiments according to the present invention. Such values can be analyzed as average values and frequency distributions from a population of individual cells.

In a particular embodiment according to the present invention, techniques for the automatic identification of mitotic cells are provided. Image analysis techniques employing techniques such as multidimensional representations, frequency-based representations, multidimensional cluster analysis techniques and the like can be included in various embodiments without departing from the scope of the present invention. Techniques for performing such analyses are known in the art and include those embodied in MatLab software, produced by MathWorks, a company with headquarters in Natick, MA.

Scalar values providing efficacious descriptors of cell images can be identified using the techniques of the present invention to perform predictive analysis of drug behavior. In a presently preferred embodiment, a plurality of heterogenous scalar values can be combined to provide predictive information about substance and cell interactions.

Fig. 2E illustrates a representative work flow diagram of simplified process steps for designing and applying analysis techniques for prediction of properties of manipulations in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of claims herein. One of

ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2E illustrates an input data of descriptors of known manipulations with known properties. A step 320 of reformatting and transforming data 319 to formats suitable for analysis is performed. Additionally, a "cleaning", or "cleansing" step can eliminate outlying and/or incomplete data points and the like in the data. Than at step 322 a set of models is being built based on data from step 320. Performance of each of these models is evaluated at step 324 and steps 320, 322, and 324 are repeated until a desired performance and error rates are achieved. Data transformations and prediction methods, including a particular neural network, mathematical equation, classification and decision trees and/or the like, that satisfy these criteria are selected at step 326 and a solution based on these transformations and methods is generated at step 328. Formatting and transformations, based upon procedures and parameters selected in step 326, are applied to descriptors of unknown manipulations 318 at step 330. Reformatted and transformed data from step 330 is analyzed using a generated solution 328, and predictions about unknown manipulations are generated at step 316, based on this analysis (332) and known properties of know manipulations 317.

Fig. 2F illustrates a representative block flow diagram of simplified process steps for a method of mapping a manipulation of cells to a morphological characteristic in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2F illustrates a step 250, wherein a plurality of cells, e.g., living cells, fixed cells or dead cell fractions, cell substructures, cell components are provided. Then, in a step 252, the plurality of cells is manipulated, where manipulation occurs using a source(s) from one or a combination selected from an electrical source, a chemical source, a thermal source, a gravitational source, a nuclear source, a temporal source, and a biological source. Next, in a step 254, a morphological value is captured from the plurality of cells. The morphological value can include one or any combination of characteristics such as a cell count, an area, a perimeter, a length, a breadth, a fiber length, a fiber breadth, a shape factor, an elliptical form factor, an inner radius, an outer radius, a mean radius, an equivalent radius, an equivalent sphere volume, an equivalent prolate volume, an equivalent oblate volume, an equivalent sphere surface area, an average gray value, a total gray value, and an optical density. Then, in a step 256, a degree of presence of the morphological value is assigned. In a step 258, the morphological value

from the plurality of cells is stored in a memory location. From the memory location the values can be used for a statistical analysis to produce a statistical profile.

Fig. 2G illustrates a representative block flow diagram of simplified process steps for populating a database with manipulated biological information, e.g., cellular enzymatic activities, cellular cascades, cellular promoters, transcription factors, translation factors, cell cycle stage and apoptosis, in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2G illustrates a step 260, wherein a plurality of cells in various stages of the cell cycle, such as for example, interphase, G0 phase, G1 phase, S phase, G2 phase, M phase, which itself includes prophase, prometaphase, metaphase, anaphase, and telophase, are provided. Then, in a step 262, each of the cells in the various stages of the cell cycle is manipulated. Next, in a step 264, an image of the plurality of manipulated cells is captured using image acquisition techniques in order to provide a morphometric value for the manipulated cells. Finally, in a step 266, a database is populated with the morphometric value. The database can later be queried based upon the morphometric value.

Fig. 2H illustrates a representative block flow diagram of simplified process steps for a method for populating a database with manipulated biological information, e.g., image acquisition parameters, image feature summary information, and well experimental parameters in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2H illustrates a step 280 in which cells are placed into site on a plate and a manipulation is applied. Then, in a step 281 an image is taken of the cells. In step 282, the image is transferred to an image archive database. Then, in a step 283, well experimental parameters are entered into the database 287. Well experimental parameters can include cell type, manipulation and the like. In a step 284, image acquisition parameters are transferred to database 287. Image acquisition parameters can include file name, fluorophores and the like. In a step 285, the image acquired in step 281 is analyzed. Then, in step 286, an image feature summary from the analysis step 285 is transferred to database 287.

In step 288, a lookup table for all analyses is provided to database 287. The lookup table provides information about the analyses. In a step 289, a query of

database 287 for process data is performed. The results are reformatted. Then in a step 290, the database 287 is queried. Next, in a step 291, features of the manipulations stored in the database are combined and reduced. Next, in a step 293, reduced features of step 291 can be compared. In a step 292, the results of step 293 are recorded in database 287. Then, in a step 294, a report of predictions based on comparisons performed in step 293 is generated.

Fig. 2I illustrates a representative block flow diagram of simplified process steps for acquiring images of manipulated biological information, e.g., cells, cell tissues, and cell substituents in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2I illustrates a step 270 in which a user sets up an image analysis procedure. Then, in a step 272, an image is read into image analysis software. Next, in a step 274, patterns and objects are identified in the image using one or more algorithms. Next, in a step 276, sets of features are extracted from the image. Then, in a step 278, feature information, descriptor values and the like are exported to the database, such as database 287 of Fig. 2H, for recording. Next, in a decisional step 279, a determination is made whether any more images should be taken. If this is so, processing continues with step 272. Otherwise, image acquisition processing is completed.

Fig. 2J illustrates a representative block flow diagram of simplified process steps for populating, acquiring and analyzing images of manipulated biological information in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2J illustrates a step 300 of placing a plate onto an imaging stage and reading a bar code. Then, in a step 301 an autofocus procedure is performed. Next, in a step 302, a first optical filter configuration is selected and an image is collected. Then, in a decisional step 303, a determination is made whether more than one image per optical configuration can be taken. If so, then, in a step 304, a new position within the well is targeted and another image is collected. Then, in a decisional step 305, a determination is made whether any more images need to be collected. If this is so, step 304 is repeated until all images for a particular well have been collected. After one or more images are collected for the well, in a step 306, the stage is returned to a starting position within the

well, and a montage is created from collected images. The results are named with a unique file name and stored.

In a decisional step 307, a determination is made whether any more optical channels in the well can be imaged. If this is so, then in a step 308 the next optical filter configuration is selected and an image is collected. Processing then continues with decisional step 303, as described above. Otherwise, if no further optical channels in the well can be imaged, then in a decisional step 309 a determination is made whether any wells remain to be imaged. If not all wells have been imaged, then in a step 310, the stage moves to the next well and processing continues with step 301, as described above. Otherwise, if all wells on the plate have been imaged, then in a decisional step 311, a determination is made whether any more plates can be processed. If this is so, then processing continues with step 300 as described above. Otherwise, in a step 312, the information is stored to a CD or other storage device as a backup.

Fig. 2K illustrates a representative block flow diagram of simplified process steps compound based upon information about effects of one or more known compounds on a cell population in a particular embodiment according to the present invention. This diagram is merely an illustration and should not limit the scope of the claims herein. One of ordinary skill in the art would recognize other variations, modifications, and alternatives. Fig. 2K illustrates a step 340 of populating a database with descriptors for known compounds. Such descriptors can be determined from imaging the cell population. However, in some embodiments, descriptors can be derived by measurements and combinations of measurements and the like. Then, in a step 342, descriptors for the unknown compound are determined from imaging a second cell population. The second cell population has been treated with the unknown compound. Then, in a step 344, a relationship between the descriptors determined from the unknown compound with the descriptors determined from the known compounds can be determined. Finally, in a step 346, an inference can be made about the unknown compound based upon the descriptors of the known compounds from the relationship determined in step 344.

Accordingly, the present invention provides a novel database design. In a particular embodiment according to the present invention, a method for providing a database comprises measurement of a potentially large number of characteristics of one or more sub-cellular morphometric markers. Markers can be from any of a large variety of normal and transformed cell lines from sources such as for example, human beings,

fungi, or other species. The markers can be chosen to cover many areas of cell biology, such as, for example markers comprising the cytoskeleton of a cell. The cytoskeleton is one of a plurality of components that determine a cell's architecture, or "cytoarchitecture". A cytoarchitecture comprises structures that can mediate most cellular processes, such as cell growth and division, for example. Because the cytoskeleton is a dynamic structure, it provides a constant indication of the processes occurring within the cell. The cytoarchitecture of a cell can be quantified to produce a one or more scalar values corresponding to many possible cellular markers, such as cytoskeleton, organelles, signaling molecules, adhesion molecules and the like. Such quantification can be performed in the presence and absence of drugs, peptides, proteins, anti-sense oligonucleotides, antibodies, genetic alterations and the like. Scalar values obtained from such quantification can provide information about the ongoing cell biological function and physiologic state of the cell.

In a presently preferred embodiment, scalar values can comprise morphometric, frequency, multi-dimensional parameters and the like, extracted from one or more fluorescence images taken from a number of cellular markers from a population of cells. A vector of two or more such scalar values extracted from a plurality of cell lines and markers grown in the same condition together comprise a unique "fingerprint" that can be incorporated into a database. Such cellular fingerprints will change in the presence of drugs, peptides, proteins, antisense oligonucleotides, antibodies or genetic alterations. Such changes can be sufficiently unique to permit a correlation to be drawn between similar fingerprints. Such correlations can predict similar behaviors or characteristics with regard to mechanism of action, toxicity, animal model effectiveness, clinical trial effectiveness, patient responses and the like. In a presently preferred embodiment, a database can be built from a plurality of such fingerprints from different cell lines, cellular markers, and compounds having known mechanisms of action (or structure, or gene response, or toxicity).

The present invention also provides database and finger print comparisons according to other embodiments. In a particular embodiment according to the present invention, measurement of scalar values can provide predictive information. A database can be provided having one or more "cellular fingerprints" comprised of descriptors of cell substance interactions of drugs having known mechanisms of action with cells. Such fingerprints can be compared using a plurality of techniques, such as a technique of creating "phylogenetic trees" of a statistical similarity between the cellular fingerprints

from various drugs. In a present embodiment, scalar, numeric values can be converted into a nucleotide or amino acid letter. Once converted into a corresponding nucleotide representation, the fingerprints can be analyzed and compared using software and algorithms known in the art for genetic and peptide sequence comparisons, such as GCG, a product of Genetics Computer Group, with company headquarters in Madison WI. In an alternative embodiment, numeric values for the fingerprints can be used by comparison techniques. A phylogenetic tree can be created that illustrates a statistical significance of the similarity between fingerprints for the drugs in the database. Because the drugs used to build the initial database are of known mechanism, it can be determined whether a particular scalar value in a fingerprint is statistically predictive. Finally, a compound fingerprint with no known mechanism of action can be queried against the database and be statistically compared and classified among the drugs in the database that the compound most resembles.

In a particular embodiment, relationships between measured morphological properties of images and physiological conditions can be determined. Relationships can include, for example, treatment of different cell lines with chemical compounds, or comparing cells from a patient with control cells, and the like. In a presently preferable embodiment, a clustering can be performed on acquired image feature vectors. Some embodiments can comprise statistical and neural network - based approaches to perform clustering and fingerprinting of various features. The foregoing is provided as merely an example, and is not intended to limit the scope of the present invention. Other techniques can be included for different types of data.

In some embodiments, clustering and fingerprinting can be performed on features extracted from cell images. In a presently preferable embodiment, procedures for comparisons and phylogenetic analysis of biological sequences can be applied to data obtained from imaging cells.

Embodiments can perform such analysis based upon factors such as numerical value, statistical properties, relationships with other values, and the like. In a particular embodiment, numbers in a numerical features vector can be substituted by one or more of nucleic acid or amino acid codes. Resulting "pseudo-sequences" can be subjected to analysis by a sequence comparison and clustering program.

Other types of databases can also be provided according to other embodiments. The database includes details about the behavior of a plurality of standard drugs of known mechanism in the universal assay, called a morphometric cellular

response. However, the comparative value need not be limited to drugs having a known mechanism of action. When the profile of a test compound is compared to the database, predictions about the test compound can be made against any known parameter of the other compounds in the database. For example, information about a compound in the database could include structure, mechanism of action, clinical side effects, toxicity, specificity, gene expression, affinity, kinetics, and the like. The fingerprint of a compound of unknown structure from a natural products library could be compared to the fingerprint of drugs with known structure and the structure could be deduced from such a comparison. Similarly, such information could lead to better approaches to compound analoging, pre-clinical animal modeling, clinical trial design (side effects, dose escalation, patient population) and the like.

According to the present invention, databases can be integrated with and complementary to existing genomic databases. Differential genomic expression strategies can be used for drug discovery using database technology. In one particular embodiment, cell data and morphometric cellular response data can be associated with a genetic expression profile assay to form a single assay. Live cells expressing fluorescence markers can be treated with a drug, imaged and analyzed for morphometry; and then analyzed for mRNA for expression. Such embodiments can provide rapid development of tools to link cellular behavior with genomics.

Database methods according to the present invention can be used to predict gene function and to assist in target validation. Databases that include genetic diversity, i.e., having cellular fingerprints from cells of differing genetic backgrounds (tumor, tissue specific, and gene knock out cell lines), can provide the capability to compare cells of unknown genetic background to those in the database. Similarly, fluorescent patterns of an unknown cellular marker in the presence of multiple drugs can be queried against the patterns of the known markers in the database. For example, if an unknown gene is tagged with Green Fluorescent Protein (GFP), the database may be used to identify the cellular structures for which that unknown gene encodes.

According to the present invention, target validation and cell-based assay screening can be performed using database system and methods to serve as a universal high-throughput cell-based assay that can evaluate the molecular mechanism of drug action. As new genes are isolated and identified, a large collection of available gene based knowledge is becoming available. From this large collection of new genes, potential targets can be identified using the genomic tools of sequence analysis and

expression profiling. However, unless a gene mutation is tightly linked to a disease state, further validation of individual targets is a time consuming process, becoming a bottleneck in drug discovery. Furthermore, robotics and miniaturization are making "High Throughput Screening (HTS)" the industry standard, substantially reducing the time and cost of running a target-based biochemical assay. Therefore, it is now be possible to routinely screen large libraries and use a resulting "hit" to validate the target. In such approaches, a specialized cell-based assay would be developed to test hits for each target. Since this often involves the creation of cell lines expressing new markers, this stage may also become a bottleneck that cannot keep pace with HTS. In addition, these assays may not be amenable to high-throughput screening, making it difficult to test the increasing number of analogs arising from combinatorial chemistry.

In a particular embodiment according to the invention, a rapid characterization of large compound libraries for potential use as pharmaceutical products can be provided by predicting compound properties such as mechanisms of action. In many drug discovery situations, virtually millions of compounds can be passed through an HTS assay against one or two validated targets. These assays produce hundreds to thousands of potential hits that can be narrowed down to a selective few. These hits can then be subsequently screened by a pipeline of secondary and tertiary screens to further characterize their specificity, often time completely missing non-specific interactions with other proteins. Techniques according to the present invention can provide a replacement to such screening operations by providing information about cellular accessibility and mechanism of action for the substances usually placed on HTS systems. The cell information can be predictive of whether to continue into an animal model for each compound, and which animal model to pursue.

In some embodiments, techniques according to the present invention can provide tools for the later stages of drug development such as clinical trial design and patient management. The predictive value of the known drug trial and patient response information will be used in a similar fashion as the pre-clinical information. Because the human cell is the locus of drug action, a database containing cellular interactions can be able to provide predictive value for this aspect of drug development.

EXPERIMENTS

To prove the principle and demonstrate the objects of the present invention, experiments have been performed to determine the effects of manipulations on

cell structure based upon imaging techniques applied to a variety of indications. These experiments were performed by growing multiple cell lines in the presence of multiple compounds, or substances. A fix and stain of cells using antibodies or labels to multiple cellular markers was performed. One or more images of the cells were then obtained using a digital camera. Indications were built by quantifying and/or qualifying patterns of each marker in the cell lines under study. A database was built from the indications.

As the database grows, it should be able to predict the mechanism of action and other compound properties of an unknown drug by comparing its effect with the effects of known compounds or to identify data clusters within large libraries of compounds.

In a first experiment, an automated method to count the number of cells and differentiate normal, mitotic, and apoptotic cells was created. Approximately 5,000 HeLa cells were plated per well in a 96 well plate and grown for 3.5 days. The cells were fixed with –20° MEOH for 5 minutes, washed with TBS for 15 minutes, and then incubated in 5 mg/ml Hoechst 33342 in TBS for 15 minutes. Then, 72 images were collected with a 40x objective and 75 ms exposure time.

The analysis was performed on objects that met a certain size criteria that was based on 1) measuring the size of objects in the image that were clearly not cells and 2) excluding the first peak of the area histogram.

Histograms of the individual object data were generated for each type of information. Fig. 3A shows the histogram for average gray value, and Fig. 3B shows histogram data for the area of each object. Fig. 3C shows the scatter plot of the average gray value vs. the area of all of the objects. The pattern of the scatter plot showed an interesting pattern: a large cluster of cells in one region of the graph, with a scattering of object points in other regions. Because mitotic structures are identified as particularly bright objects, most likely due to the biological fact that the chromatin is condensed, it seemed reasonable to go back to the original Hoechst images and the identify the cells which were either undergoing mitosis, or otherwise looked abnormal. Manual inspection of 917 cells resulted in the classification of each object. Fig. 3D shows a graph where each type of cellular classification is delimited. This graph clearly shows that the mitotic nuclei are exclusively brighter than the interphase nuclei. Further, the different phases of the cell cycle can be separated using these two parameters. Figs. 3E-3F show the bar graphs of the average and standard deviations of the areas and average gray values for

each cell classification type. These graphs shows that interphase nuclei are statistically less bright than mitotic nuclei and that telophase nuclei are statistically smaller than other mitotic nuclei.

Each image was thresholded to a level of 20. A standard area value was set at 9500 pixels. Automated information gathering about all of the objects was done and collected into an Excel spreadsheet (for more information see, section on imaging system). The following information was recorded:

Image Name	**Average gray value**
Object #	Total gray value
Area	Optical density
Standard area count	Radial dispersion
Perimeter	Texture Difference Moment
Fiber length	EFA Harmonic 2, Semi-Major Axis
Fiber breadth	EFA Harmonic 2, Semi-Minor Axis
Shape factor	EFA Harmonic 2, Semi-Major Axis Angle
Ell. form factor	EFA Harmonic 2, Ellipse Area
Inner radius	EFA Harmonic 2, Axial Ratio
Outer radius	EFA Harmonic 3, Semi-Minor Axis
Mean radius	

The following results were obtained:

- 1,250 objects were counted
- 201 of those objects has standard area counts > 2 (area > 19000 pixels)
- 195 objects had areas < 6000 pixels
- 1529 objects estimated in total
- 1328 object areas are > 6000 pixels
- The data was reduced to 917 objects that were 6000 < area < 19000
- For the 917 objects a scatter plot of area vs. average gray value and a histogram of the average gray value were generated.
- 116 objects that had average gray value intensities > 60 were manually looked at to determine their morphology.
- Of those 116 objects:

6 were dead or indistinguishable

4 were interphase

30 were prophase

32 were metaphase

24 were anaphase

20 were telophase (10 pairs)

- 12 prophase objects were missed because of gray scale cut off. (8 of those prophase cells had gray scale values > 57, as did 7 interphase)
- 1 telophase object was missed because it was too small (<6000)
- 1 prophase object was missed because it was too big (>1900)
- 16 mitotic objects were missed because they were parts of objects with standard count > 2.

In sum, out of 917 single objects, the analysis correctly identified 106 out of 130 mitotic objects, or (81% predictive, 91% of identified mitotics). Out of 917 single objects, the analysis incorrectly identified only 10 non-mitotics as mitotics (1% total, 8% of identified mitotics); 14 mitotics as interphase (1.4% total, 1% interphase).

The next step is to develop an automated classification system which will automatically assign values to each object using these or other measurement parameters.

In a second experiment, the effects of Taxol on MDCK cells and the different types of morphological effects were observed. A plurality of MDCK cells grown in 96 well plates were treated with Taxol for 4.5 hours at different concentrations (10 uM-1pM). They were then fixed, labeled with Hoechst, and imaged.

This experiment used a labeling protocol comprising: MEOH fix at –20°, Wash in PBS, Block in PBS/BSA/Serum/Triton-X 100, Incubate with 5 μg/ml Hoechst 10 minutes, and Wash.

The results of the experiment are that cells were inspected for different morphologies and manually counted at each different drug concentration in one well. Fig. 4 shows example images from each drug concentration and the different types of morphologies are highlighted. Fig. 5 shows the distribution of each morphology within the cell population as a function of drug concentration. The higher the concentration of Taxol, the larger proportion of cells underwent apoptosis, and the fewer number of normal mitotic cells were detected.

The next step is to test the automated Hoechst analysis of the first experiment with multiple drugs.

In a third experiment, the purpose is to determine whether the automated analysis methods developed in the first experiment can detect differences in Hoechst morphology in the presence of 6 known compounds at one concentration and exposure time in one cell line. In this experiment, HeLa cells were treated with 6 compounds with known mechanism of action. The quantitative methods described in the first experiment were applied to the Hoechst images.

Approximately 5,000 HeLa cells per well were plated in a Costar black walled 96 well tissue culture treated plate and left to recover in the incubator for 24 hours. After this time, 10 ug/mL of cytochalasin D (CD), Taxol, hydroxyurea, vinblastine, and nocodazole, and staurosporine was added to different wells at a 1:100 addition in DMSO. The cells were incubated in the presence of drug for 24 more hours. After 24 hours, the cells were removed and fixed as in the first experiment. Then, 9 images per well were collected of the Hoechst staining using a 10x objective.

The results of this experiment were that the low magnification images taken of Hoechst were run through the automated image analysis method described in the first experiment. Plots of the average gray value and area were made of each compound. Fig. 6 shows the scatter plots of the compounds. The scatter plots of each compound are visually distinct. For example, cells treated with CD are smaller than control, and cells treated with Hydroxyurea are larger and brighter. Furthermore, the number of cells per well was very different (data not shown).

Based upon the results of this experiment, it can be concluded that these initial attempts at automatically identifying changes in cellular morphology demonstrate that the effects of different compounds can be distinguished. This method can also be used to count adherent cells.

The next steps that can be taken based upon the results of this experiment are to develop clustering algorithms that will assign statistically meaningful values to the representative two dimensional data shown in Fig. 5, and even more complicated clustering of all of the multidimensional data that can be extracted across one, and multiple markers.

In a fourth experiment was performed to obtain high magnification images of two markers in the presence of drugs. In this experiment, HeLa cells were treated with

80 generic compounds with known mechanism of action. The quantitative methods described in the first experiment were applied to the Hoechst images.

Approximately 5,000 HeLa cells per well were plated in a Costar black walled 96 well tissue culture treated plate and left to recover in the incubator for 24 hours. After this time, 10 ug/mL of each compound from the Killer Plate from Microsource Discovery Systems (Gaylordsville, CT) was added to different wells at a 1:100 addition in DMSO. The cells were incubated in the presence of drug for 24 more hours. After 24 hours, the cells were removed and fixed as in the first experiment. In addition to being labeled with Hoechst 33342 (against chromatin), cells were also labeled with 1 unit of rhodamine-conjugated phalloidin (against actin) for 30 minutes.

The 96 well plate was imaged twice. Once, 9 images per well were collected of the Hoechst staining using a 10x objective. After this, one image per well of both the phalloidin and Hoechst staining was collected using a 40x objective.

The resulting high magnification images were analyzed qualitatively and distinct pattern differences were detected in both the Hoechst and phalloidin images. Fig. 7 shows three example images from the experiment. The top row is the Hoechst staining, and the bottom row is the phalloidin staining from the same well. The columns show the images from wells treated with just DMSO (control), cytochalasin D, and Colchicine. Notice that the morphology of each marker is different in the presence of each drug. Interestingly, there is an effect in the morphology of the chromatin in the Hoechst image of cytochalasin D, which effects the actin cytoskeleton (and thus there is an expected effect in the phalloidin image). Also, there is an effect on the actin cytoskeleton, compared to control, in the presence of colchicine that effects the microtubule network.

The low magnification images were analyzed as described in the first experiment, and different patterns were seen in both the average gray value vs. area plots, and in the number of cells per well (data not shown). Based upon the results of this experiment, it can be concluded that the fact that changes in patterns of a marker that is "down-stream" from the mechanism of action of a compound are detectable illustrates the efficacy of this approach.

The next step based upon the results of this experiment is to develop automated image analysis protocols for actin and other markers.

A fifth experiment was performed to test quadruple labeling of 9 different cell lines grown in normal conditions. In this experiment, NCI-H460, A549, MDA-MD-

231, MCF-7, SK-OV-3, OVCAR-3, A498, U-2 OS, and HeLa cells were plated. Then, the cells were fixed and stained for DNA, tubulin, actin, and Golgi markers.

The following table summarizes the procedures for this experiment:

Action	Active Ingredient/Notes	Buffer	Vol/ well	Desired Time	Temp
Remove media	NOTE: gently by pipetting, not aspiration				
Fix	4% Formaldehyde	PBS	100μl	20 min	rt
Wash		TBS	100μl	5 min	rt
Wash		TBS	100μl	5 min	rt
Permeablize	0.1% Triton X-100	TBS	100μl	10 min	rt
Permeablize	0.1% Triton X-100	TBS	100μl	10 min	rt
Block	% BSA % Serum Filter sterilize before use	TBS w/azide	100μl	1hr or o/n	rt or 4°C
Primary Antibody	1:1000 dilution of DM1α	TBS + 1% BSA + 0.1% TX-100	50μl	1hr or o/n	rt or 4°C
Wash		TBS	100μl	5 min	rt
Wash		TBS	100μl	5 min	rt
Wash		TBS	100μl	5 min	rt
Fluorescent Stain	FITC lens culinaris 1:500 Rhodamine-Phalloidin 1:500 CY5 goat anti-mouse 1:100	TBS + 1% BSA + 0.1% TX-100	50μl	1 hr.	rt, dark
Wash		PBS	100μl	5 min	rt, dark
Hoechst	1:1000 dilution of 5mg/ml	TBS	100μl	15 min	rt, dark
Wash		PBS	100μl	5 min	rt, dark
Wash		PBS	100μl	5 min	rt, dark
Wash		PBS	100μl	5 min	rt, dark
Store		PBS	200μl	1 month	4°C

Cells were plated out at different densities for 48 hours. Cells were fixed and labeled by the above method. Cells were imaged using an automated imaging macro that collected 9 images from each marker using a 10x objective. Higher magnification images were collected of a few cells for demonstration purposes.

In this experiment, each cell line demonstrated different morphological patterns as determined by phase. For example, A549 cells are much more compacted than OVCAR-3 cells as determined by phase contract imaging (data not shown). The different fluorescent markers showed even bigger differences between different cell lines. Figs. 8 and 9 show 4 panels of each marker for A549 (Fig. 8) and OVCAR-3 cells (Fig. 9). The markers are Hoechst (upper left), Phalloidin (upper right), Lens culinaris (lower left), and DM1a antibody (lower right). The following table summarizes the qualitative differences between these images:

Marker	A549	OVCAR3
Hoechst/DNA	small	large
Phalloidin/actin	fuzzy	crisp - many stress fibers
Lens culinaris/Golgi	compact	Disperse/punctate
DM1alpha/Tubulin	perinuclear	evenly distributed

Higher magnification images were taken of the OVCAR3 cells. Fig. 10 shows the same markers at 20x, and Fig. 11 shows the markers at 40x. While the highest magnification images show the most detail, these images illustrate that very little morphological information is lost in the 10x images.

These data exemplify the differences in morphology seen between different cell types. Thus the automated image analysis software will have to be customized for each marker in each cell type. Different drugs should effect these morphologies differentially.

The next steps based upon the results of this experiment are to customize and develop an automated quantification for each marker and cell line.

A sixth experiment was conducted with a more sophisticated software package and to develop more flexible image recognition algorithms. In this experiment, prototype image features extraction was performed using Matlab programming language with image toolbox and SDC morphology toolboxes. Algorithms are being developed that will automatically identify objects on images and to measure various morphological and intensity parameters of these objects. Since at present it is not known which of the measurements will be most useful for subsequent clustering, many different measurements for each of the cellular markers were acquired.

An example of a MatLab program called "AnalyseDNA" that takes as an input an unlimited number of images, identifies individual objects in these images based on either their intensities, or based on edge-detection algorithms, and extracts a number of morphological and intensity characteristics of these objects is provided in a particular embodiment according to the present invention. It will be understood that other programs could also be used in other embodiments without departing from the scope of the present invention. Thus, the copy of this program reproduced below is intended to be representative but not limiting:

Listing of the AnalyseDNA.m program and of some of the supporting subroutines

```
function files_analysed = AnalyseDNA(filemask, outpath, nx,
ny, filter_range, dext, modifier, sfname)
% AnalyseDNA performs measurements on files of DNA images
% V1. EV 2-11-99; 2-15-99; 2-16-99
%
% files_analysed = AnalyseDNA(filemask, outpath, nx, ny,
filter_range, dext, modifier, sfname)
%
% PARAMETERS:
%    ALL PARAMETERS ARE OPTIONAL
%
%    FILEMASK - mask for file names to be analyzed
INCLUDING PATH(for example c:\images\*.tif)
%    DEFAULT '.\*.tif' (all *.tif files in the current
directory).
%
%    OUTPATH - path to a directory where all the output
files will be placed.
%    DEFAULT - output is saved in the same directory which
contains images
%
%    NX, NY - number of individual images in montage images
along X and Y axes (DEFAULT 1)
%
%    FILTER_RANGE - 3 col-wide array (or[]). Specifies how
data is filtered when summary is calculated
%    this parameter internally is passed to GetDNAData and
then to GetSummaryData - see these
%    functions for details. For example: [2 2 Inf; 6 100
8000] will case all raws of data for which
%         values in column 2 are less than 2 and all raws
where values in column 6 are less than 100 or
%         more than 8000 to be excluded from all
calculations of a summary.
%    DEFAULT - [] (means do not filter, summarize all data)
%
%    DEXT - string. Extension for data files being saved.
%    DEFAULT 'dat';
%
%    MODIFIER - this modifier is 'SUMMARY', summary file is
created;
%         'SUMMARY ONLY' - only summary is generated, data
for individual files are not saved
%
%    sfname - string. File name of a summary file
```

```
%    DEFAULT 'summary[date].dat'
%
% OUTPUT:
%
%    AnalyseDNA works on image files or montages. For each
image file it creates a tab-delimits file of measured
%    parameters of all the objects in the montage with the
same base name as a montage file and extension specified
%    by dext parameter (or .dat by default) and file
'errors[date].err' - with the list of files that matched the
%    filemask but could not be processed.
%    If 'summary' or 'summary only' modifier is specified,
it also creates a single file 'summary[date].dat' (or
%    different extension, if specified by DEXT) which
contains summary information for all analyzed files.
%
%    ALL OUTPUT FILES are saved in a directory specified by
OUTPATH parameter
%
%    RETURNS *files_analysed* - number of files that have
been successfully processed.
%
%    Column designations in the output files are described
in GetDNAData
%
% FILE NAME CONVENTIONS
%    AnalyseDNA attempts to identify a number for each file
to identify the file in summary output.
%    It does that by looking for the first space or
underscore, followed by a number and then takes
%    as many successive numbers as it can find. If it fails
to identify a number it assigns a
%    default which is -1
%
%
% SEE ALSO GetDNAData, GetSummaryData
%
% TO DO   improve error handling in opening and writing
files (GLOBAL error_file ?)
%         include procedures for writing text headers into
the output files

if nargin > 8
   error ('Wrong number of input parameters');
end
if nargout >1
   error ('Wrong number of output parameters: only one
allowed');
end

% set defaults
```

```
need_summary = 0;
summary_only = 0;
use_default_outpath = 0;
datestring = datestr(floor(now));
if nargin == 7      % set default summary file name
   sfname = ['summary' deblank(datestring)]; % extension
will be appended later based on dext
   if  deblank(upper(modifier)) == 'SUMMARY'
      need_summary = 1;
   elseif deblank(upper(modifier)) == 'SUMMARY ONLY'
      need_summary = 1;
      summary_only = 1;
   else
      error (['Wrong parameter: unknown modifier '
modifier]);
   end
end

if nargin == 5
   % default data file extension
   set dext = 'dat';
end
if nargin == 4
   % default filter range
   filter_range = [];
end
if nargin == 3
   ny = 1; % default number of images in montage along Y
end
if nargin == 2
   nx = 1;
end
if nargin == 1
   use_default_outpath = 1;
end
if nargin == 0
   filemask = '*.tif'
end

% check parameters
if ( ~ischar(filemask) |  ~ischar(dext) | ~ischar(sfname) )
      error('Wrong parameter type: filename, filepath,
dext and sfname should be strings');
end
if ( ( size(nx) ~= [1 1] ) | ( size(ny) ~= [1 1] ) )
   error ('Wrong parameter type: nx and ny should be scalars
(1x1 arrays)');
end
if (~isempty(filter_range) & size(filter_range, 2) ~= 3)
   error ('Wrong parameter type: filter range should be []
or 3 - cols-wide array');
```

```
end
% end testing parameters

% Generate list of files to process

datapath = getpath(filemask);
if use_default_outpath == 1
   outpath = datapath;
end
if exist(outpath, 'dir') ~= 7
   error(['Path ' outpath, 'not found. Exiting..']);
elseif exist(datapath, 'dir') ~= 7
   error(['Path ' datapath, 'not found. Exiting..']);
end

sfname = makefullname(outpath, sfname, dext);
if need_summary == 1
   if exist(sfname, 'file')
      disp(['File ', sfname, 'already exists!']);
      input ('Press ^C to abort, Enter to delete and
continue');
      delete(sfname);
   end
end


flist = FileList(getfname(filemask), datapath);
numfiles = size(flist, 1); % total number of files to
process
disp(['About to process ', num2str(numfiles), ' files']);
%DEBUG  - commented out "input" to run from Wrod
input('Press ^C to abort, Enter to continue');

% main loop where the job gets done:
error_file = makefullname(outpath, ['error' datestring
'.err']);
num_processed = 0;
num_error =0;
for i = 1:numfiles
     % first generate file name for a data output file
   current_fullname = flist(i, :); % full name with path and
extension
   current_datafile = makefullname(outpath,
makefname(getbasefname(current_fullname), dext) );

   %extract number from a filename
   fnumber = getfilenumber(current_fullname);

   % load an imagefile, record errors
   read_error = 0;
   try
```

```
         I = imread(current_fullname);
         %DEBUG
         disp (['Image file #', num2str(fnumber), ' loaded']);
   catch
      % record file-opening error in an error_file
      read_error = 1;
      num_error = num_error +1;
      msg = [current_fullname ': ' lasterr];
      add_error_msg(error_file, msg);
   end

   % extract and write data to a file in outpath
   if read_error ~=1
      if (need_summary == 0)
         %DEBUG
         disp (['Starting analysis of file #',
num2str(fnumber), '.']);
         current_data = GetDNAData(I, nx, ny, fnumber);
         %DEBUG
         disp (['Finished analysis of file #',
num2str(fnumber), '.']);
         %load current_data.mat 'current_data';
         write_data(current_data, current_datafile);
      else     %summary needed
         %DEBUG
         [current_data, current_summary] = GetDNAData(I, nx,
ny, fnumber, filter_range);
         %load current_data.mat 'current_data';
         %load current_summary.mat 'current_summary';
         write_summary (current_summary, sfname);
         if summary_only ~= 1
            write_data(current_data, current_datafile);
         end
      end
   end
end % of the main for loop
num_processed = numfiles - num_error;

%=======================end function AnalyseDNA()
=======================================

%============================================================
============================
function result = add_error_msg(filename, msg)
% adds string MSG to an errorfile FILENAME
% returns 1 if success, 0 if failure

err_FID = fopen(filename, 'at');
if err_FID == -1
   warning(['Can not open error file ' filename]);
else
```

```
   fprintf(err_FID, '%s\n', msg);
   fclose(err_FID);
end
%=====================end function add_error_masg()
===================================

%============================================================
============================
function N = getfilenumber(fname)
% returns the first number extracted from a file name
(string) or -1 if fails to extract any number
numbers = NumbersFromString( getfname(fname) ); % vector of
all numbers encoded in the name

                    % (but not in the path, even if present)
if isempty(numbers)
   N = (-1);    % return -1 if no numbers found in the name
else
   N = numbers(1);
end

%===================== end function getfilenumber()
====================================

%============================================================
============================
function result = write_data(data_array, file_name)
% writes data in a data_array in a tab-delimited ascii file.
% result is 0 if success and -1 if failure
% if file_name exists, overwrites it
result = -1;
try
   fid = fopen(file_name, 'wt');
   if fid ~= -1
      for k = 1:size(data_array, 1)
         fprintf(fid, '%g\t', data_array(k, :) );
         fprintf (fid, '\n');
      end
      test = fclose(fid);
      result = -1;
catch
   result = -1;
end

%===================== end function write_data()
=======================================

%============================================================
============================
function result = write_summary (s_vector, file_name)
```

```
% appends summary vector s_vector to a file_name (ASCII tab-
delimited file).
% if file_name does not exist, creates it.
% result is 0 if success and -1 if failure
%
result = -1;
try
   % debug
   fid = fopen(file_name, 'at');
   result = fprintf(fid, '%g\t', s_vector);
   result = fprintf(fid, '\n');
   result = fclose(fid);
   result = 0;
catch
   result = -1;
end

% =================== end function write_summary()
====================================

function Data = GetObjectsData(I, Ilabel)
% GetObjectsData returns array measurements of objects in
image "I" masked by "Ilabel"
% EV 2-3-99; 2-10-99
% OData = GetObjectsData(I, Ilabel) returns an array of
morphological and intensity measurements
%    taken from a grayscale image "I". Objects are
identified on a mask image Ilabel, usually
%    created by bwlabel()
% OUTPUT:
% Each row in the output array OData represents individual
object
% columns  contain the following measurements:
%
%    1 - Index ("number" of an object);       8  - Solidity;
%    2 - X coordinate of the center of mass; 9  - Extent;
%    3 - Y coordinate         -"-           ; 10 - Total
Intensity;
%    4 - Total Area (in pixels);              11 - Avg.
Intensity;
%    5 - Ratio of MajorAxis/MinorAxis;        12 - Median
Intensity;
%    6 - Eccentricity;                    13 - Intensity of
20% bright pixel
%    7 - EquivDiameter;                   14 - Intensity of
80% bright pixel
%
% For details on morphological parameters see information on
MatLab imfeature();
% Intensity parameters are either obvious or are documented
in comments in this file.
```

```
% Procedures in this file are documented in notebook file
"MATLAB Measuring Nuclei (1) 1-29-98.doc"

if (nargin ~= 2)
   error ('function requires exactly 2 parameters');
end
if (nargout ~= 1)
   error ('function has 1 output argument (array X by 14)');
end

% finished checking arguments

% first collect morphological parameters in a structure
array:
ImStats = imfeature(Ilabel, 'Area', 'Centroid',
'MajorAxisLength',...
   'MinorAxisLength', 'Eccentricity', 'EquivDiameter', ...
   'Solidity', 'Extent', 8 );

% now convert it into array (matrix) while collecting
intensity data for each object:

%preallocate output array:
numobjects = size(ImStats, 1);
OData = zeros(numobjects, 14);
%now convert ImStats into array and add intensity data to it
for k=1:numobjects
     OData(k, 1) = k;
     OData(k, 2) = ImStats(k).Centroid(1);
     OData(k, 3) = ImStats(k).Centroid(2);
     OData(k, 4) = ImStats(k).Area;
     OData(k, 5) = (ImStats(k).MajorAxisLength) /
(ImStats(k).MinorAxisLength);
     OData(k, 6) = ImStats(k).Eccentricity ;
     OData(k, 7) = ImStats(k).EquivDiameter;
     OData(k, 8) = ImStats(k).Solidity;
     OData(k, 9) = ImStats(k).Extent;

     % now collect and assign intensity parameters from
image I

     object_pixels = find( Ilabel == k);
     object_area = size(object_pixels, 1); %same as total
number of pixels in the object
     object_intensities = double(I(object_pixels)); % need
to convert to double to do math
     sorted_intensities = sort(object_intensities); % will
need to get median, 20% and 80% pixels
     total_intensity = sum(object_intensities, 1);
     avg_intensity = total_intensity / object_area;
```

```
     median_intensity = sorted_intensities( floor(
object_area/2 ) + 1 );
     pix20 = sorted_intensities( floor(object_area*0.2)+1 )
; %brightest pixel among dimmest 20%
     pix80 = sorted_intensities( floor(object_area*0.8)+1 )
;

     OData(k, 10) = total_intensity;
     OData(k, 11) = avg_intensity;
     OData(k, 12) = median_intensity;
     OData(k, 13) = pix20; %brightest pixel among dimmest
20%
     OData(k, 14) = pix80; %dimmest pixel among brightest
20%
end %for

%================== end function
GetObjectsData()==============================


function Imask = MaskDNA1(I);
% MaskDNA1 - generates binary mask for cell nuclei through
edge detection
% EV 1-22-99; 2-6-99; 2-10-99
% Imask = MaskDNA1(I)
% PARAMETERS
%    I - intensity image (grayscale)
% OUTPUT
%    Imask - BW image with objects from I
%
% For more details see Notebook Matlab_DNA_masking1_1-22-
99.doc
% Uses SDC Morphology Toolbox V0.7

if (nargin ~= 1)
   error('Wrong number of input parameters');
end
if (nargout ~= 1)
   error('Wrong number of output parameters: one output
argument should be provided');
end


Imask = edge(I, 'canny');
Imask = mmdil(Imask, mmsecross(1));
Imask = mmero ( mmclohole(Imask,mmsecross(1)));
Imask = mmedgeoff(Imask, mmsecross(1));
% note that mmedgeoff this command removed FILLED OBJECTS
but not touching OUTLINES.
% these outlines can be removed by filtering:
Imask = medfilt2(Imask, [5 5]);
```

```
%=========end MaskDNA1 ==================================
```

Given the list of image files or montages of images as an input, this program creates an individual file for each image that contains the following quantitative measurements for all objects identified in the image:

1 - Index ("number" of an object);
2 - X coordinate of the center of mass;
3 - Y coordinate -"- ;
4 - Total Area (in pixels);
5 - Ratio of MajorAxis/MinorAxis;
6 - Eccentricity;
7 - EquivDiameter;
8 - Solidity;
9 - Extent;
10 - Total Intensity;
11 - Avg. Intensity;
12 - Median Intensity;
13 - Intensity of 20% bright pixel
14 - Intensity of 80% bright pixel

A fragment of an output for a single file, containing 9 images of cells stained for DNA and acquired with a 10x lens, is provided in a particular embodiment according to the present invention. It will be understood that other results could also be obtained in other embodiments without departing from the scope of the present invention. Thus, the copy of this example output file reproduced in Appendix A is intended to be representative but not limiting.

A montage image that was used as a source to generate data in Appendix A is presented in Fig. 12. The same program also summarizes measurements across many files and performs statistical analysis of the summary data. It creates a summary file with the following data:

1 - Image file number;
2 - Average object Area (in pixels);
3 - STD (standard deviation) of 2;
4 - Avg. of Ratio of MajorAxis/MinorAxis;
5 - STD of 4;
6 - Avg. Eccentricity;
7 - STD of 6;
8 - Avg. EquivDiameter;
9 - STD of 8;
10 - Avg. of Solidity;
11 - STD of 10;

12 - Avg. of Extent;	13 - STD of 11
14 - Avg. of objects Total Intensity;	15 - STD of 14
16 - Avg. of objects Avg Intensity;	16 - STD of 15
18 - Avg. of objects Median intensity;	19 - STD of 18
20 - Avg. of objects intensity of 20% bright pixel;	21 - STD of 19
22 - Avg. of objects intensity of 80% bright pixel;	23 - STD of 21

An example of summary output obtained by running AnalyseDNA against 10 montage files is provided in a particular embodiment according to the present invention. It will be understood that other results could also be obtained in other embodiments without departing from the scope of the present invention. Thus, the copy of this example output file reproduced in Appendix B is intended to be representative but not limiting.

A seventh experiment was conducted in order to use sequence analysis algorithms to analyze features of cell images. In this experiment, HeLa cells were treated for 24 hour with several different compounds, fixed, and stained with a fluorescent DNA dye. One image of these cells was acquired for each of the treatments and following morphometric parameters were measured:

Resulting measurements were arranged into a string of numbers and reduced to a pseudo- nucleic acid sequence using following rules: At any given position in the sequence a number was substituted by "t" (a code for thymidine) if its value is among highest 25% of the values at the corresponding position in the data set, "g" if it is between 50% and 25%, "c" if it is between 75% and 50%, and "a" if it belongs to lowest 25% of values. Thus one sequence was generated per treatment as illustrated in Fig. 13.

Resulting sequences were clustered using an AlignX module commercial software package Vector NTI (http://informaxinc.com), which uses a Neighbor Joining algorithm for sequence clustering.

Resulting dendrogram is presented in Fig. 13. On the dendrogram the closest "leafs" correspond to the closest pseudo-sequences. Interestingly, compounds with similar mechanisms of action cluster together on the dendrogram. Another example of the generation of pseudo-sequences and clustering is shown in Fig. 14.

CONCLUSION

Although the above has generally described the present invention according to specific computer based software and systems, the present invention has a much broader range of applicability. In particular, the present invention is not limited to a particular kind of data about a cell, but can be applied to virtually any cellular data where an understanding about the workings of the cell is desired. Thus, in some embodiments, the techniques of the present invention could provide information about many different types of cells, substances, and genetic processes of all kinds. Of course, one of ordinary skill in the art would recognize other variations, modifications, and alternatives.

APPENDIX

Data derived from select embodiments has been attached as a paper appendix, the entire contents of which is incorporated herein by reference for all purposes

WHAT IS CLAIMED IS:

1. A computer program product for populating a database with manipulated biological information, said computer program product comprising:

code for providing a plurality of cells in various stages of the cell cycle, said stages of the cell cycle including at least one selected from interphase, G0 phase, G1 phase, S phase, G2 phase, M phase, prophase, prometaphase, metaphase, anaphase, and telophase;

code for manipulating said cells in said various stages of cell cycle development to form a plurality of manipulated cells;

code for capturing an image of said plurality of manipulated cells;

code for determining a descriptor from said image for said manipulated cells;

code for populating a database with said descriptor;

wherein said image includes a first component of a cell and a second component of said cell; and

a computer readable storage medium for holding the codes.

2. The computer program product of claim 1 wherein said first component and said second component are selected from a protein, a protein modification, a nucleic acid, a lipid, a carbohydrate, a sub-cellular structure and an organelle.

3. The computer program product of claim 1 wherein said image is a digitized representation of said plurality of manipulated cells.

4. The computer program product of claim 3 wherein said digitized representation provides a density value of said plurality of manipulated cells.

5. The computer program product of claim 1 wherein said descriptors comprise numeric or logical values.

6. The computer program product of claim 5 wherein said values further comprises a nucleotide.

6. The computer program product of claim 5 wherein said values further comprises an amino acid letter.

8. A computer program product for determining a property of a manipulation based upon effects of said manipulation on at least two of a plurality of components of at least one of a plurality of cells, said computer program product comprising:

code for providing at least one of a plurality of samples of said manipulation to said at least one of a plurality of cells;

code for determining at least one of a plurality of features of said at least two of a plurality of components of at least one of a plurality of cells in the presence of said manipulation;

code for determining at least one of a plurality of descriptors, said descriptors comprising at least one of said plurality of features;

code for searching a plurality of descriptors obtained from a database to locate descriptors based upon one of said descriptors of said manipulation, said searching forming a plurality of located descriptors;

code for determining, based upon said located descriptors, properties of said manipulation based upon said located descriptors;

wherein said two of a plurality of components includes a first component and a second component of a cell, said code for determining at least one of a plurality of descriptors of a state comprises code for combining information about said first component and said second component; and

a computer readable storage medium for holding the codes.

9. The computer program product of claim 8 wherein said plurality of components are selected from a protein, a protein modification, a nucleic acid, a lipid, a carbohydrate, a sub-cellular structure and an organelle.

10. The computer program product of claim 8 wherein said code for determining said plurality of located descriptors further comprises code for determining a plurality of matching descriptors, said matching descriptors corresponding to a prior administration of said manipulation, said prior administration of said manipulation having at least one of a plurality of properties.

11. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying a chemical factor.

12. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying a biological factor.

13. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying an electromagnetic factor.

14. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying a gravitational factor.

15. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying a mechanical factor.

16. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying a thermal factor.

17. The computer program product of claim 8 wherein said manipulation comprises a temporal factor.

18. The computer program product of claim 8 wherein said code for providing a manipulation comprises code for applying a nuclear factor.

19. The computer program product of claim 8 wherein said properties comprises toxicity.

20. The computer program product of claim 8 wherein said properties comprises specificity against a subset of tumors.

21. The computer program product of claim 8 wherein said properties comprises a mechanism of chemical activity.

22. The computer program product of claim 8 wherein said properties comprises a mechanism of biological activity.

23. The computer program product of claim 8 wherein said properties comprises a target protein.

24. The computer program product of claim 8 wherein said properties comprises a mechanism of action.

25. The computer program product of claim 8 wherein said properties comprises a structure.

26. The computer program product of claim 8 wherein said properties comprises at least one of a plurality of adverse biological effects.

27. The computer program product of claim 8 wherein said properties comprises at least one of a plurality of biological pathways.

28. The computer program product of claim 8 wherein said properties comprises at least one of a plurality of adverse clinical effects.

29. The computer program product of claim 8 wherein said properties comprises at least one of a plurality of cellular availability.

30. The computer program product of claim 8 wherein said properties comprises at least one of a plurality of pharmacological properties.

31. The computer program product of claim 8 wherein said properties comprises a gene expression profile.

32. The computer program product of claim 30 wherein said pharmacological properties comprises absorption.

33. The computer program product of claim 30 wherein said pharmacological properties comprises excretion.

34. The computer program product of claim 30 wherein said pharmacological properties comprises distribution.

35. The computer program product of claim 30 wherein said pharmacological properties comprises metabolism.

36. The computer program product of claim 8 wherein said properties comprises pharmacodynamic properties.

37. The computer program product of claim 8 wherein said properties can be selected from clinical uses and indications, human and veterinary diagnostic uses and tests, or human and veterinary prognostic uses and tests..

38. The computer program product of claim 8 wherein said descriptor comprises a scalar.

39. The computer program product of claim 8 wherein said descriptor comprises a vector.

40. A computer program product of mapping a manipulation of cells based upon a morphological value, said computer program product comprising:

code for capturing a morphological value from said plurality of cells said cells being manupulated;

code for assigning a degree of presence of said morphological value; and

code for storing said morphological value and said degree of presence;

wherein said morphological value is derived from a first component of a cell and a second component of said cell, said code for capturing said morphometric value from said plurality of cells comprises code for determining a relationship between said first component and said second component; and

a computer readable storage medium for holding the codes.

41. The computer program product of claim 40 wherein said first component and said second component are selected from a protein, a protein modification, a nucleic acid, a lipid, a carbohydrate, a subcellular structure and an organelle.

42. The computer program product of claim 40 wherein said manipulation occurs in a manner selected from a electrical source, a chemical source, a thermal source, a gravitational source, a nuclear source, a temporal source, and a biological source.

43. The computer program product of claim 42 wherein said chemical source is selected from a pharmacological candidate and a drug screening library.

44. The computer program product of claim 40 wherein said morphological value is selected from a count, an area, a perimeter, a length, a breadth, a fiber length, a fiber breadth, a shape factor, a elliptical form factor, an inner radius, an outer radius, a mean radius, an equivalent radius, an equivalent sphere volume, an equivalent prolate volume, an equivalent oblate volume, an equivalent sphere surface area, an average gray value, a total gray value, and an optical density.

45. The computer program product of claim 40 wherein said degree of presence is multiple of a quantized value.

46. A computer program product of predicting properties of an unknown compound based upon information about effects of at least one of a plurality of known compounds on a first cell population, said computer program product comprising:

code for populating a database with descriptors for known compounds, wherein said descriptors are determined from imaging said first cell population;

code for determining descriptors for cells subjected to the unknown compound, wherein said descriptors are determined from imaging a second cell population;

code for determining a relationship between said descriptors of said unknown compound with said descriptors of said known compounds;

code for making an inference about said unknown compound based upon said descriptors of said known compounds; and

a computer readable storage medium for holding the codes.

47. The computer program product of claim 46 wherein said code for determining descriptors comprises code for determining a relationship between said first component and said second component.

48. The computer program product of claim 47 w herein said first component and said second component are selected from a protein, a protein modification, a nucleic acid, a lipid, a carbohydrate, a sub-cellular structure and an organelle.

A DATABASE SYSTEM INCLUDING COMPUTER CODE FOR PREDICTIVE CELLULAR BIOINFORMATICS

ABSTRACT OF THE DISCLOSURE

According to the present invention, computer based techniques for using information technology in therapeutics or drug discovery. In an exemplary embodiment, computer based techniques for determining information about the properties of substances based upon information about structure of living or non-living cells exposed to substances are provided. Computer software according to the present invention enables researchers and/or scientists to identify promising candidates in the search for new and better medicines or treatments using, for example, a cellular informatics database.

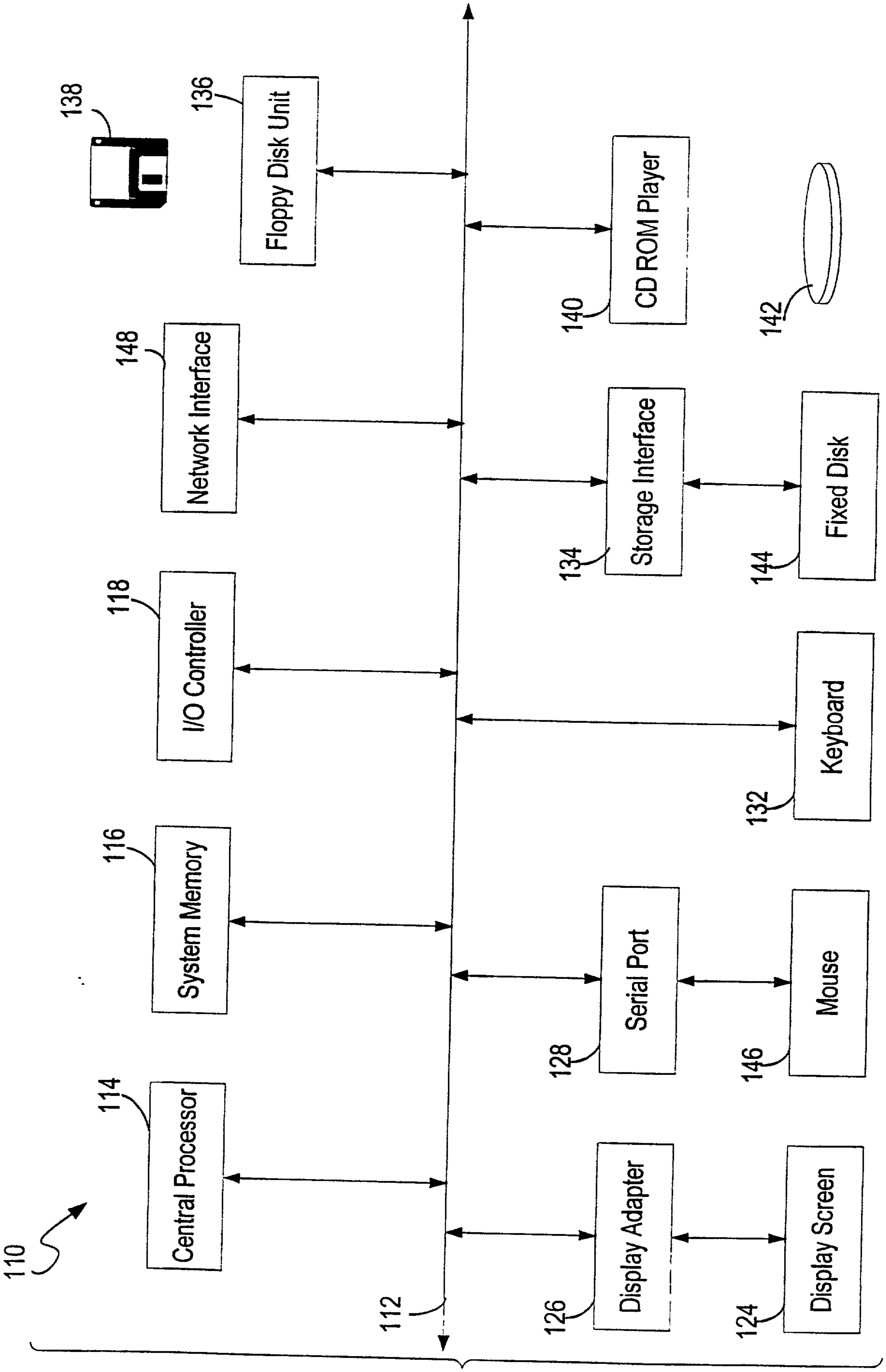

110
Central Processor
114
System Memory
116
I/O Controller
118
Network Interface
148
Floppy Disk Unit
136
138
112
Display Adapter
126
Serial Port
128
Storage Interface
134
CD ROM Player
140
Display Screen
124
Mouse
146
Keyboard
132
Fixed Disk
144
142

Fig. 1

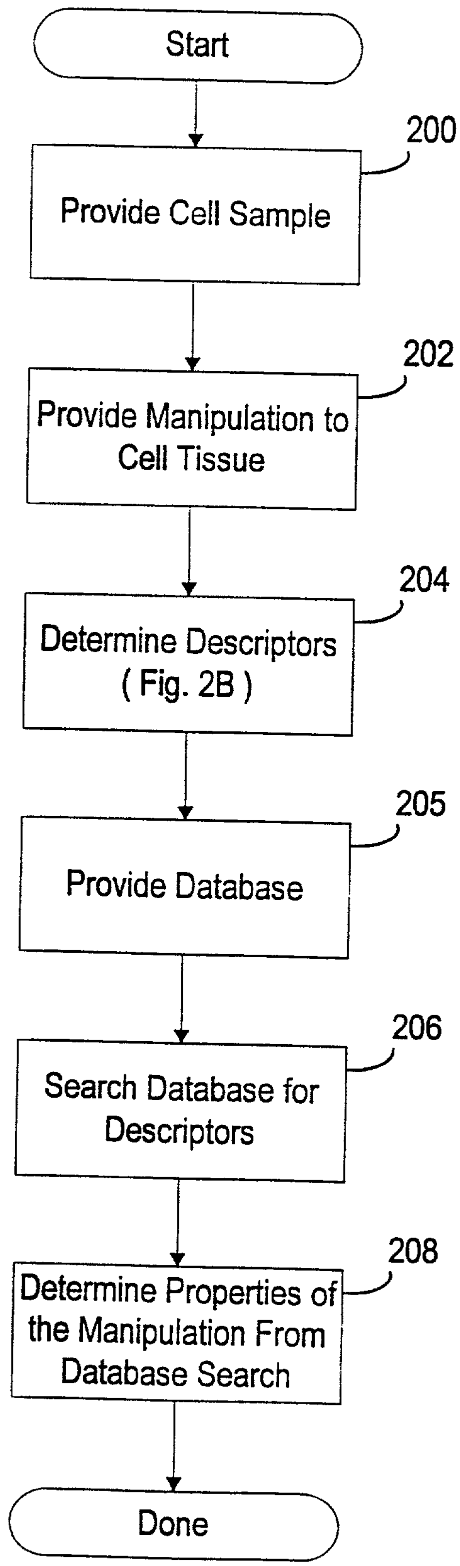

Start
Provide Cell Sample
200
Provide Manipulation to Cell Tissue
202
Determine Descriptors (Fig. 2B)
204
Provide Database
205
Search Database for Descriptors
206
Determine Properties of the Manipulation From Database Search
208
Done

Fig. 2A

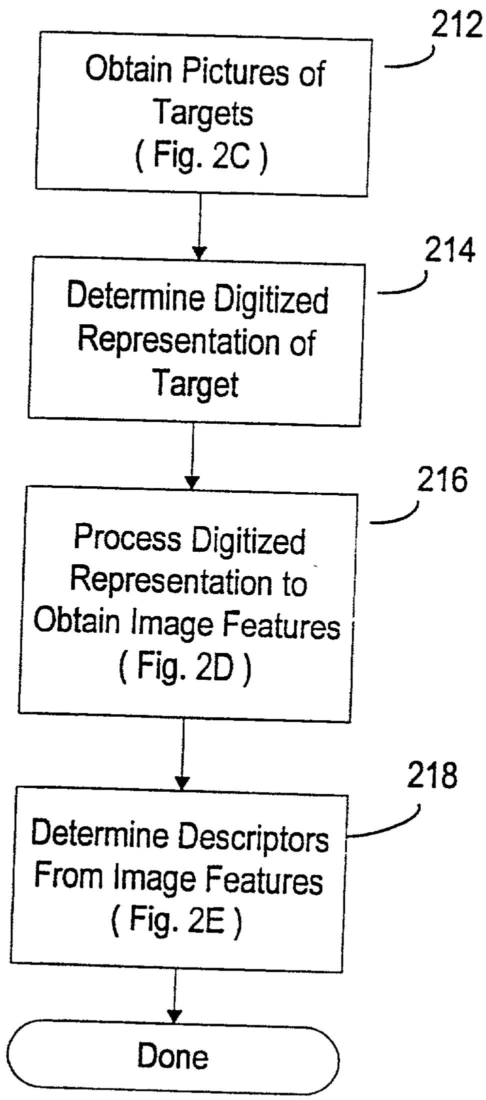


Fig. 2B
Step 204 of Fig. 2A

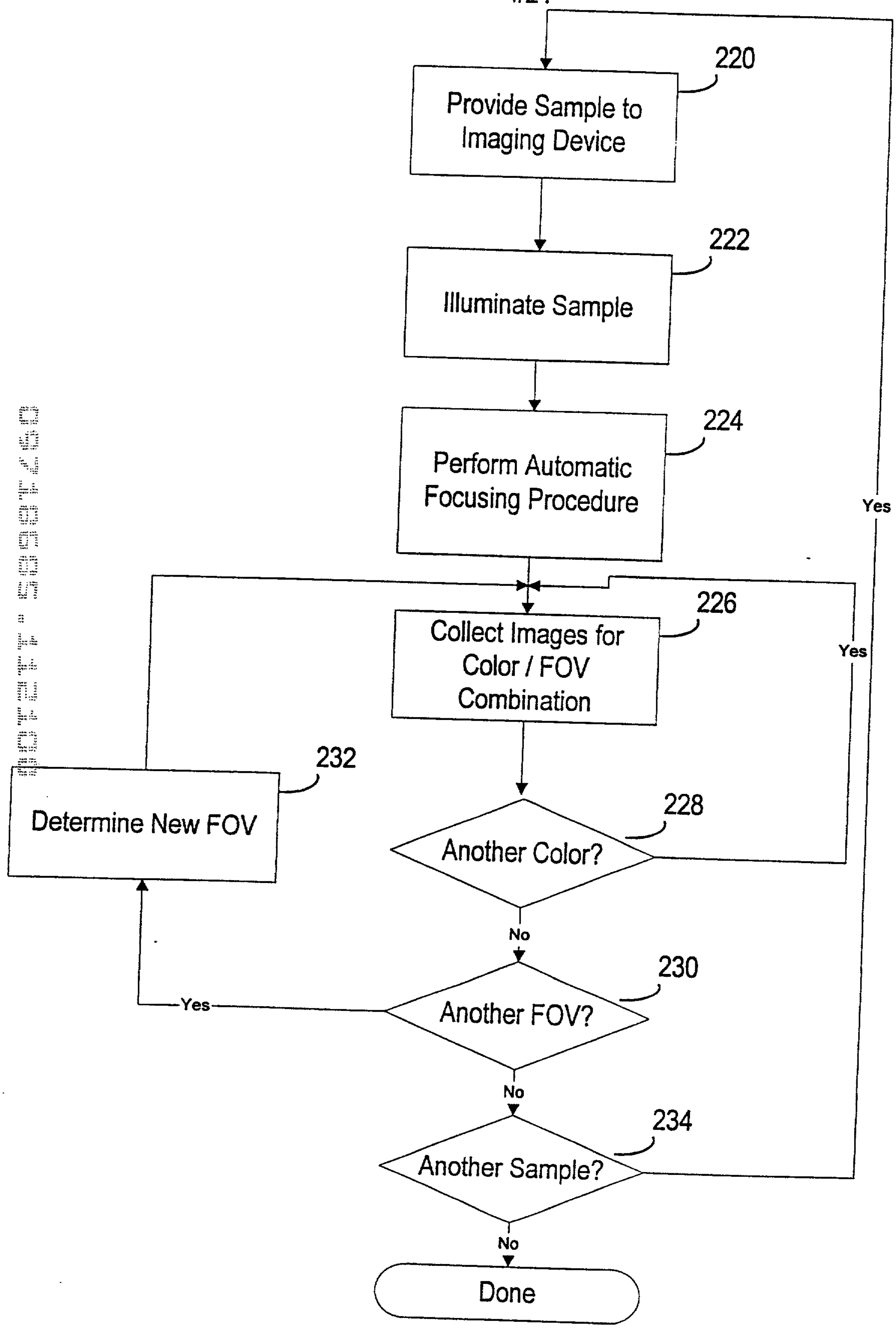


Fig. 2C
Step 214 of Fig. 2B

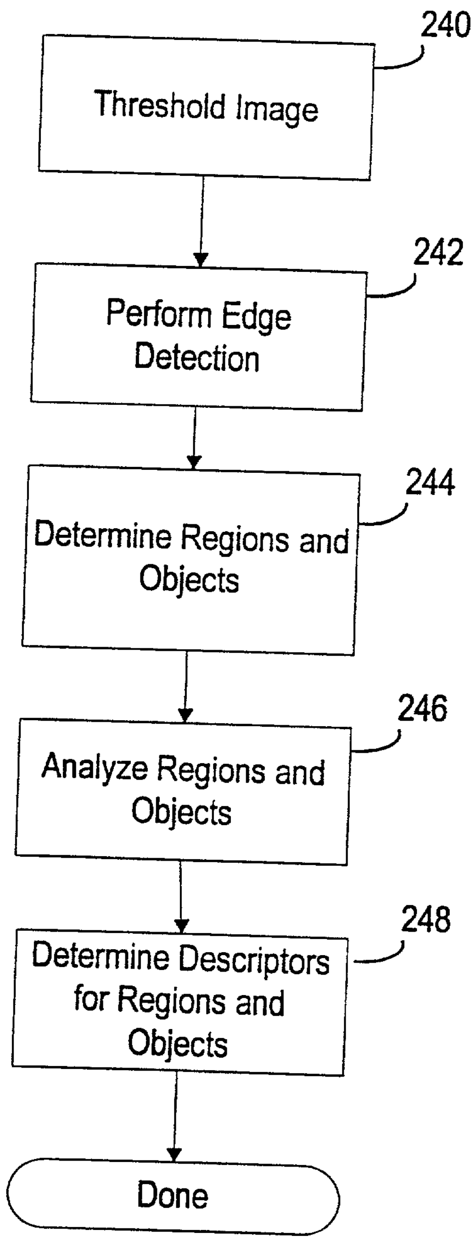
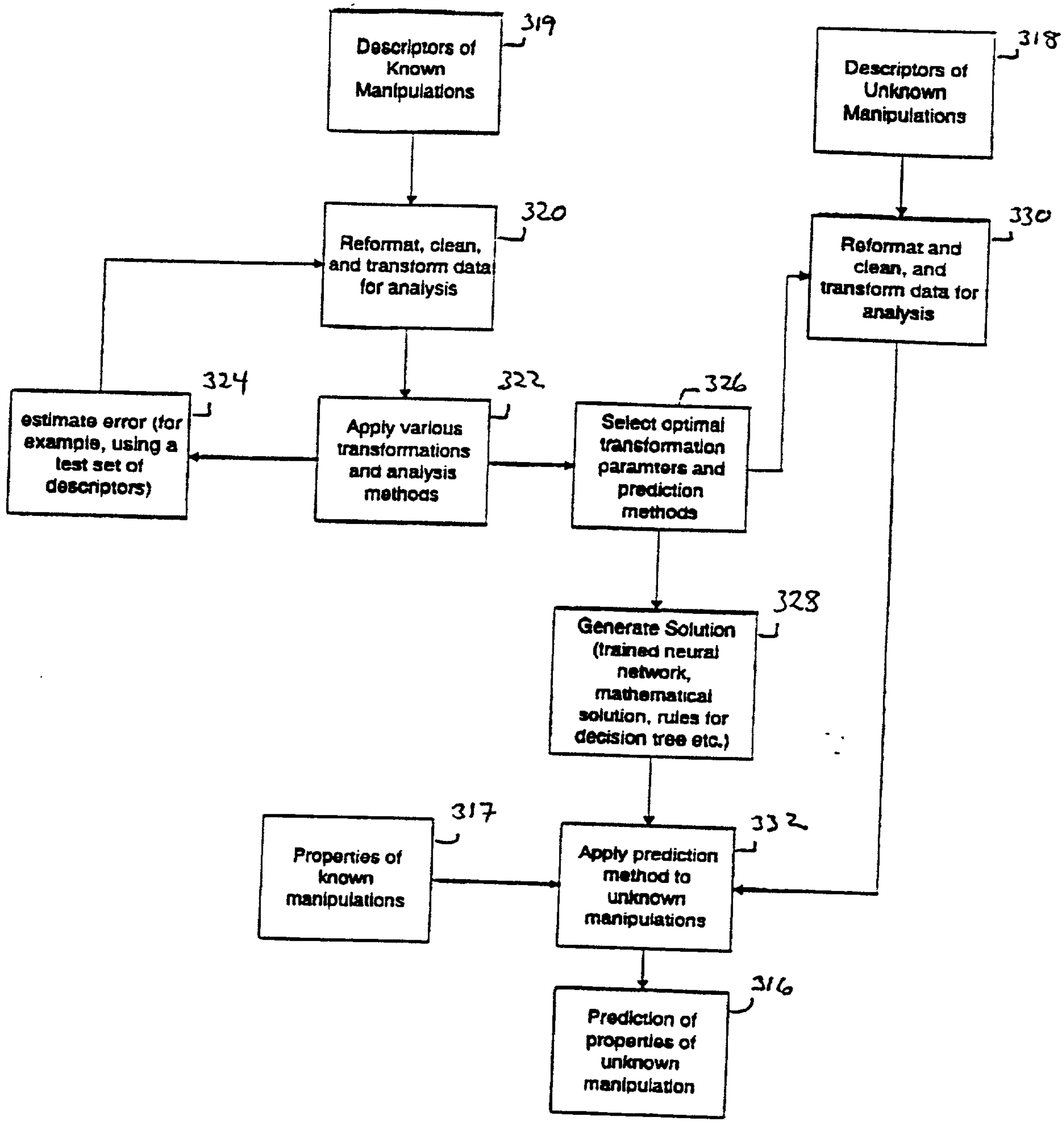


Fig. 2D
Step 216 of Fig. 2B



319
Descriptors of Known Manipulations
318
Descriptors of Unknown Manipulations
320
Reformat, clean, and transform data for analysis
330
Reformat and clean, and transform data for analysis
324
estimate error (for example, using a test set of descriptors)
322
Apply various transformations and analysis methods
326
Select optimal transformation paramters and prediction methods
328
Generate Solution (trained neural network, mathematical solution, rules for decision tree etc.)
317
Properties of known manipulations
332
Apply prediction method to unknown manipulations
316
Prediction of properties of unknown manipulation

FIG 2E

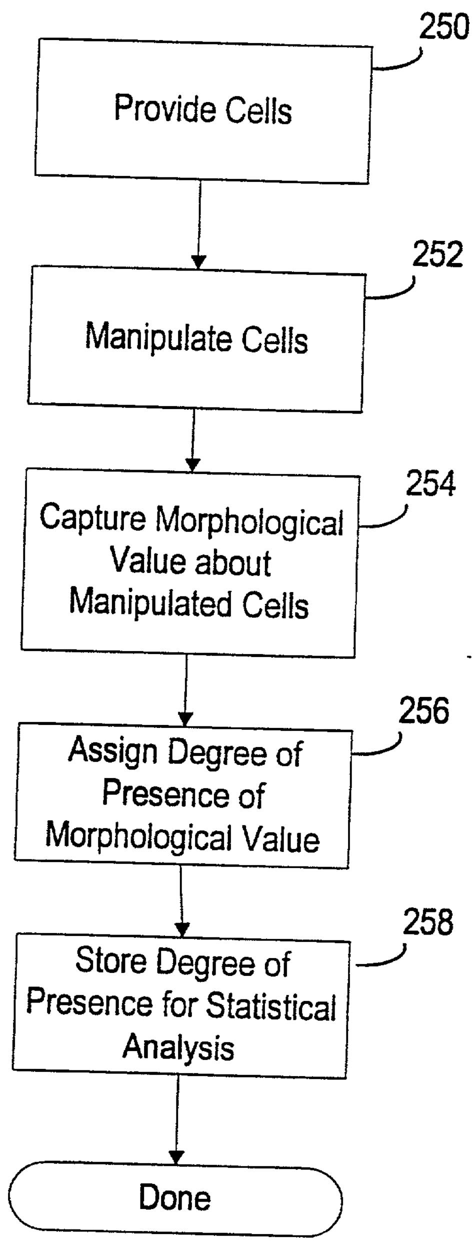

250
Provide Cells
252
Manipulate Cells
254
Capture Morphological Value about Manipulated Cells
256
Assign Degree of Presence of Morphological Value
258
Store Degree of Presence for Statistical Analysis
Done

Fig. 2F

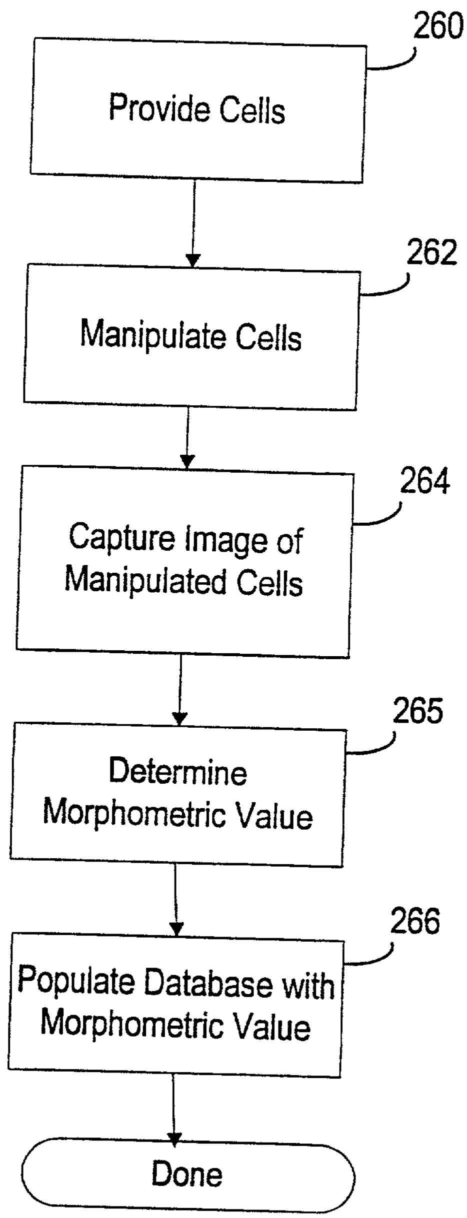

260
Provide Cells
262
Manipulate Cells
264
Capture Image of Manipulated Cells
265
Determine Morphometric Value
266
Populate Database with Morphometric Value
Done

Fig. 2G

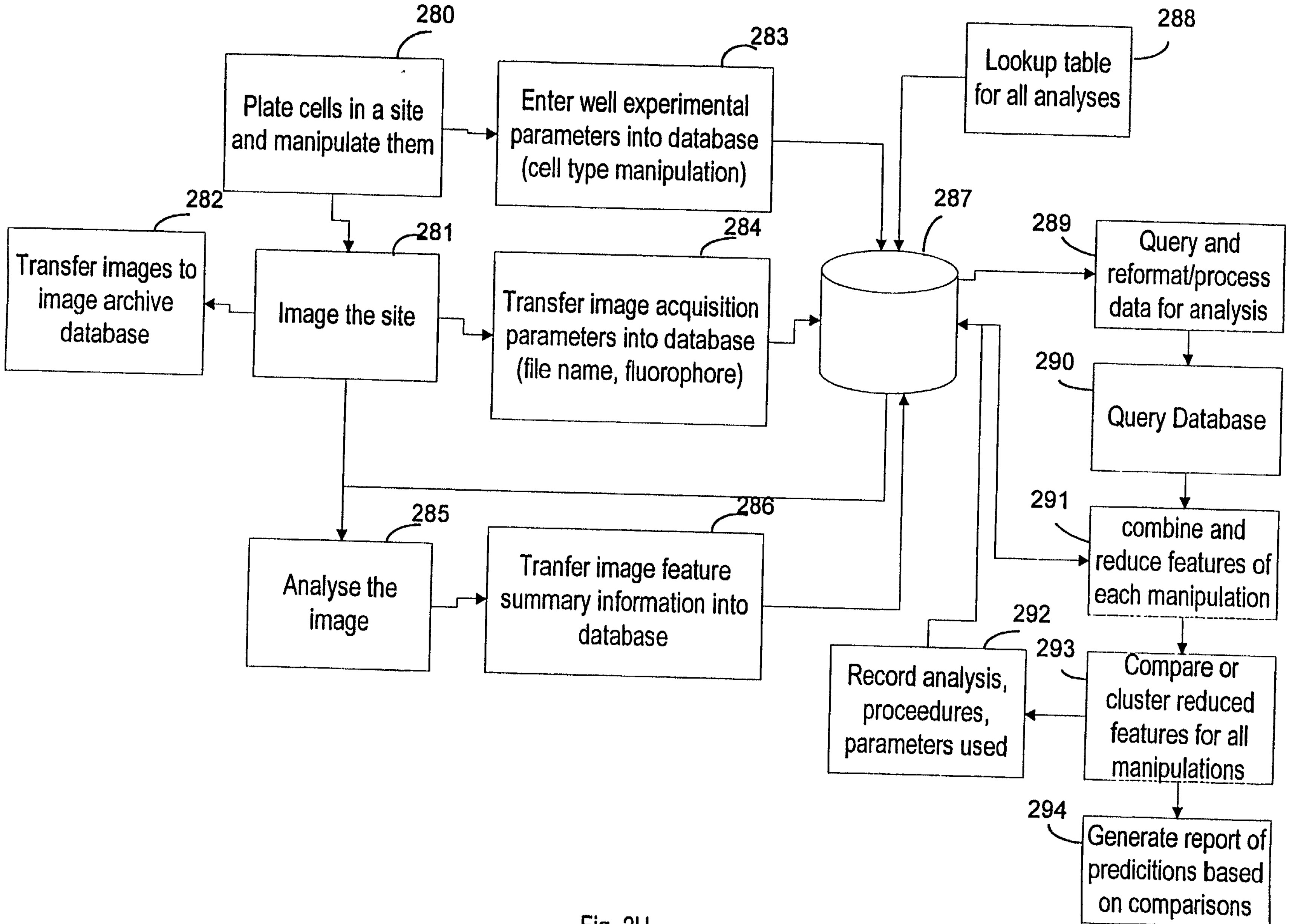

280
Plate cells in a site and manipulate them
283
Enter well experimental parameters into database (cell type manipulation)
288
Lookup table for all analyses
282
Transfer images to image archive database
281
Image the site
284
Transfer image acquisition parameters into database (file name, fluorophore)
287
289
Query and reformat/process data for analysis
290
Query Database
291
combine and reduce features of each manipulation
285
Analyse the image
286
Tranfer image feature summary information into database
292
Record analysis, proceedures, parameters used
293
Compare or cluster reduced features for all manipulations
294
Generate report of predicitions based on comparisons

Fig. 2H

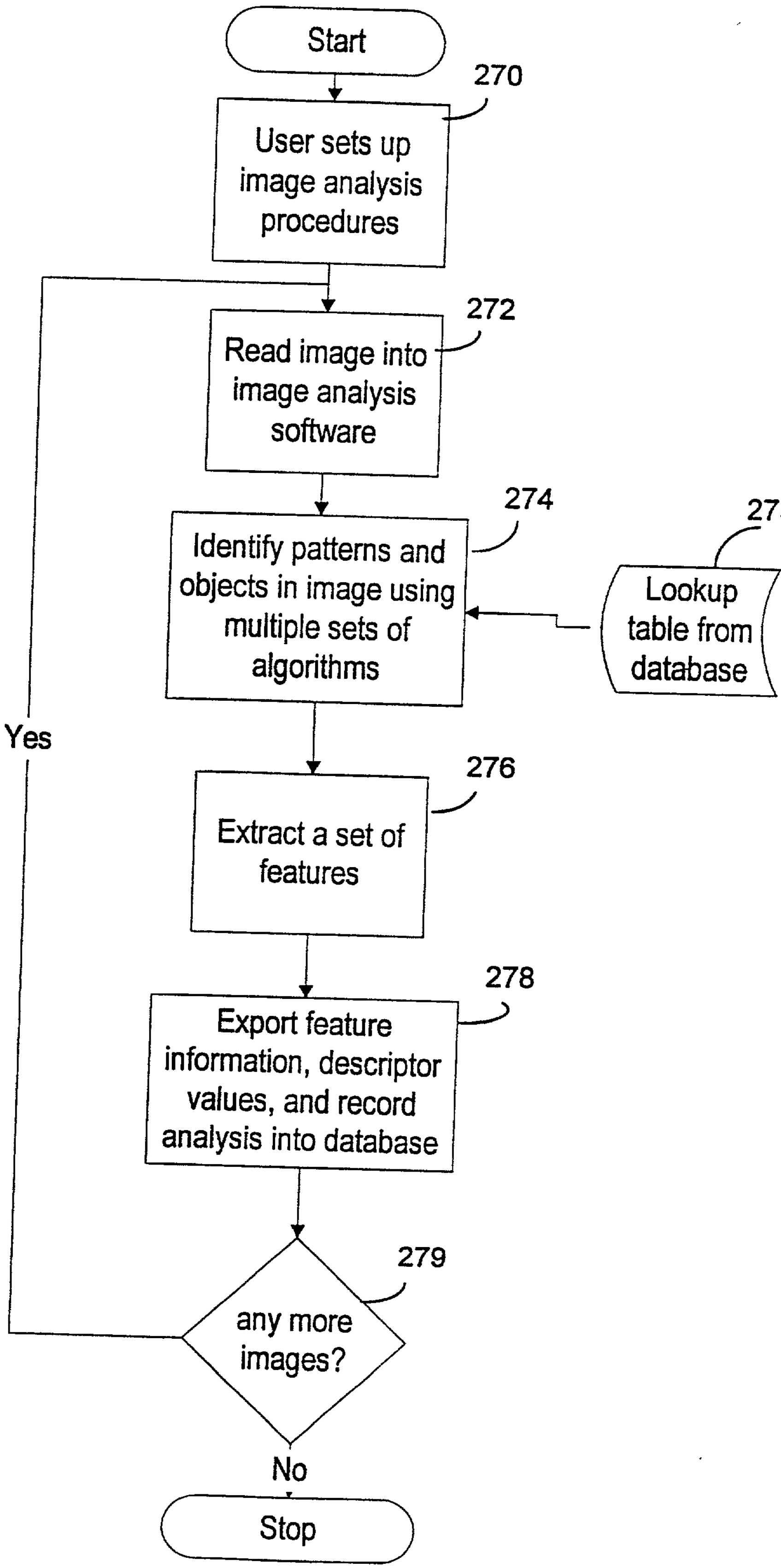

Start
270
User sets up image analysis procedures
272
Read image into image analysis software
274
Identify patterns and objects in image using multiple sets of algorithms
275
Lookup table from database
Yes
276
Extract a set of features
278
Export feature information, descriptor values, and record analysis into database
279
any more images?
No
Stop

Fig. 2I

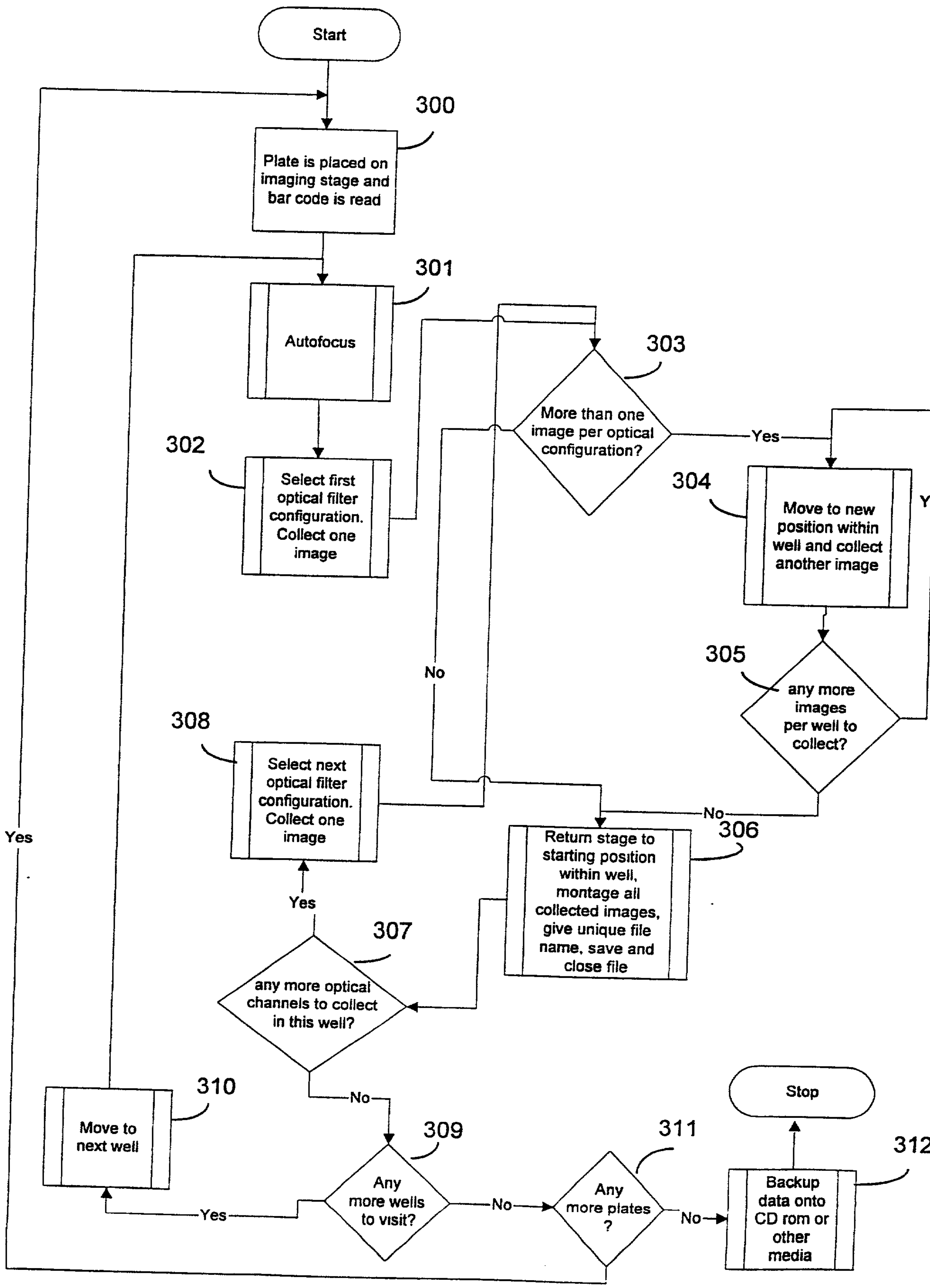

Start
300
Plate is placed on imaging stage and bar code is read
301
Autofocus
302
Select first optical filter configuration. Collect one image
303
More than one image per optical configuration?
Yes
304
Move to new position within well and collect another image
Yes
305
any more images per well to collect?
No
No
308
Select next optical filter configuration. Collect one image
306
Return stage to starting position within well, montage all collected images, give unique file name, save and close file
Yes
Yes
307
any more optical channels to collect in this well?
No
310
Move to next well
309
Any more wells to visit?
Yes
No
311
Any more plates ?
No
Stop
312
Backup data onto CD rom or other media

Fig. 2J

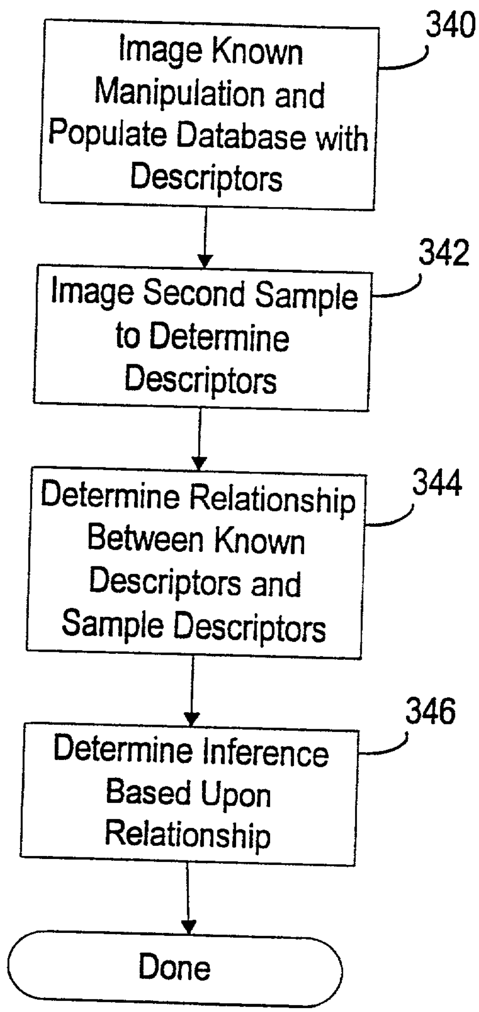


Image Known Manipulation and Populate Database with Descriptors
340
Image Second Sample to Determine Descriptors
342
Determine Relationship Between Known Descriptors and Sample Descriptors
344
Determine Inference Based Upon Relationship
346
Done

Fig. 2K

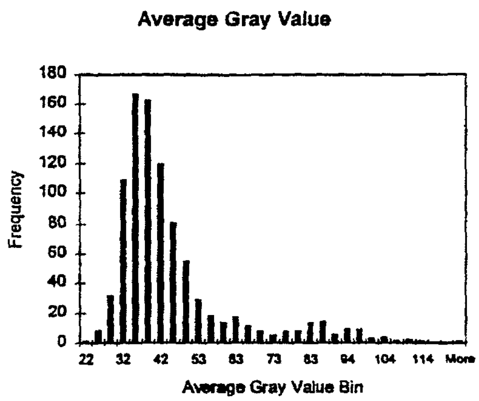


Fig. 3A

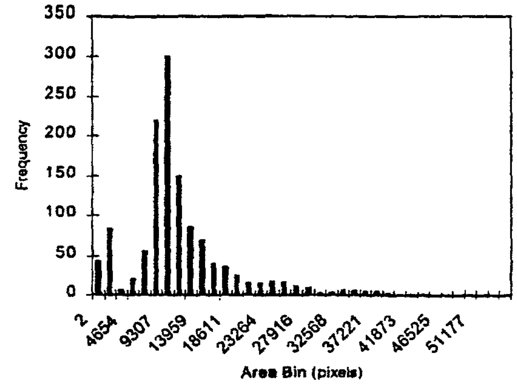


Fig. 3B

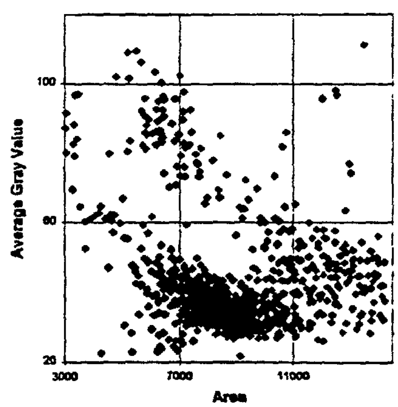


Fig. 3C

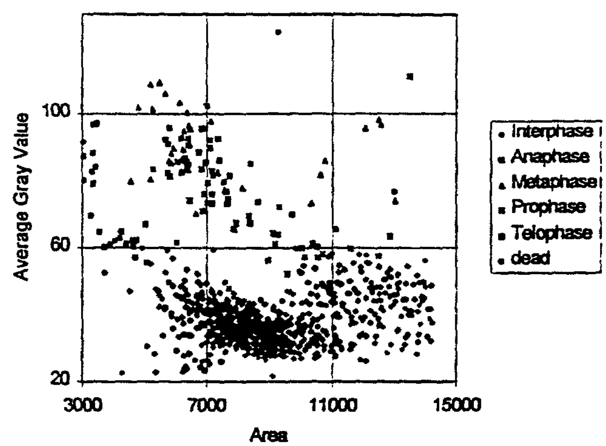


Fig. 3D

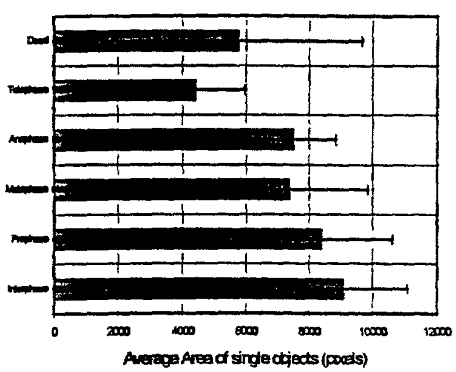


Fig. 3E

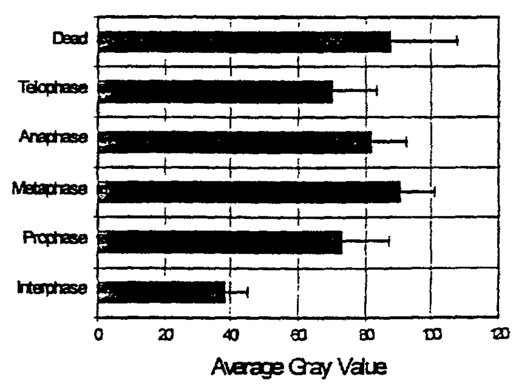
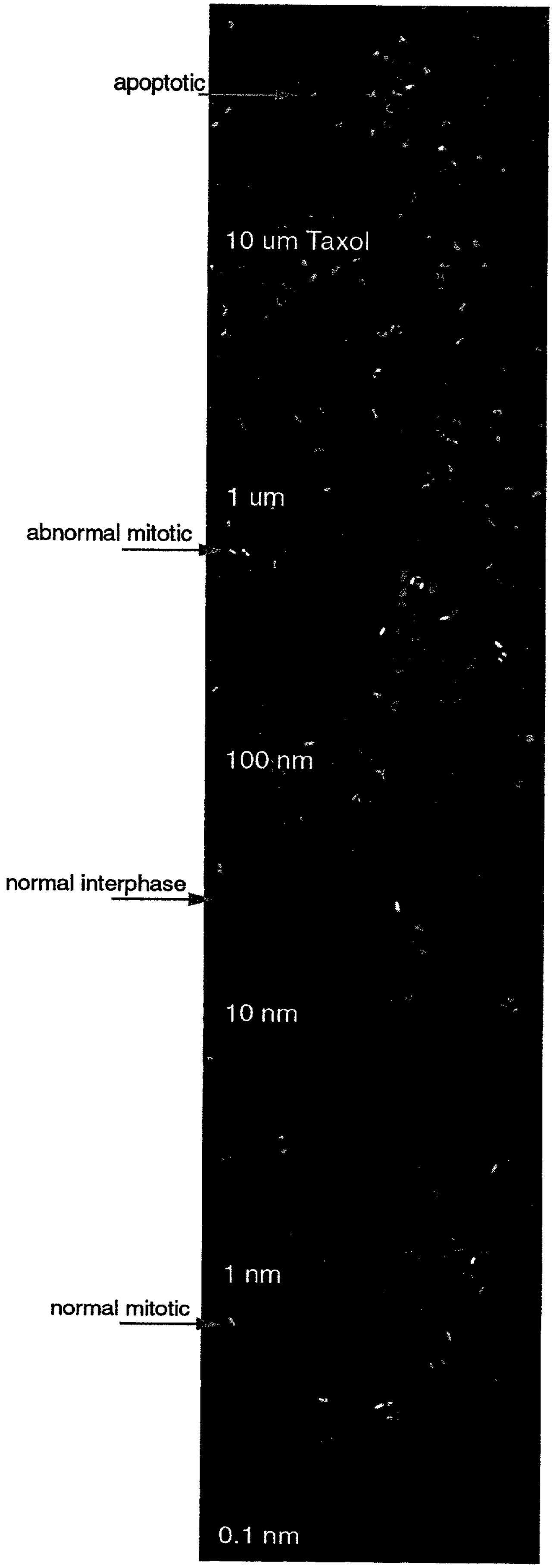


Fig. 3F

FIG. 4


apoptotic
10 um Taxol
1 um
abnormal mitotic
100 nm
normal interphase
10 nm
1 nm
normal mitotic
0.1 nm

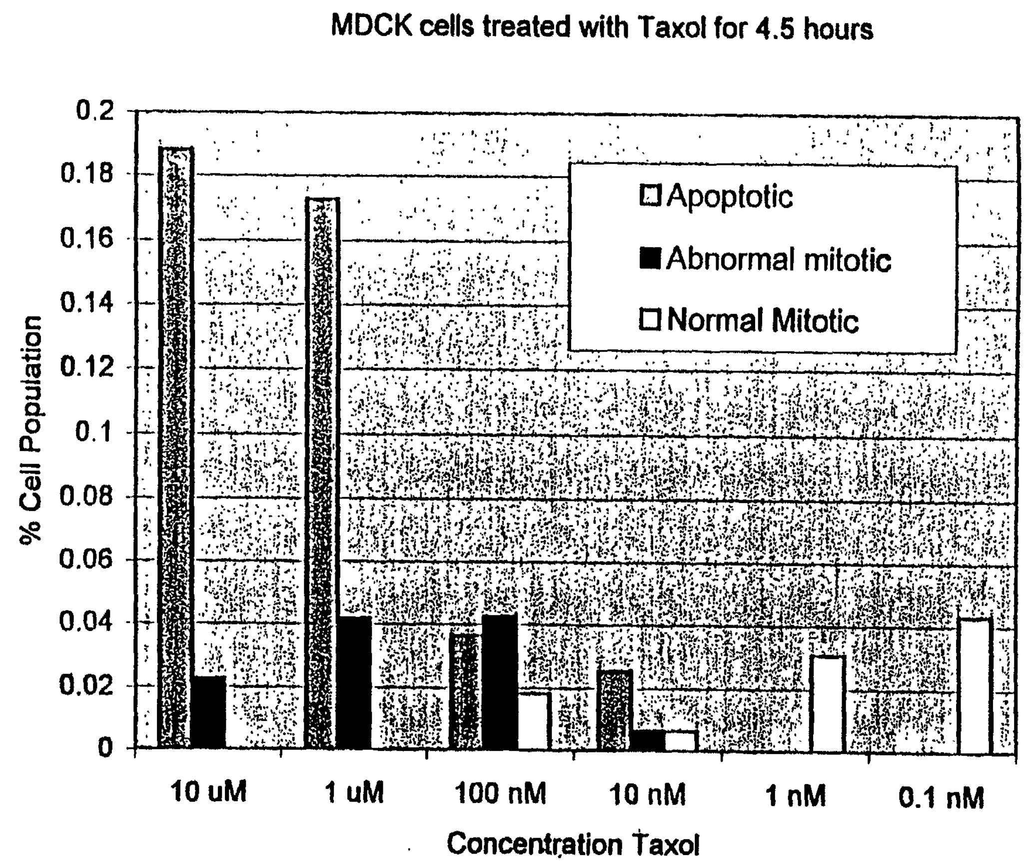

MDCK cells treated with Taxol for 4.5 hours
0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
% Cell Population
Apoptotic
Abnormal mitotic
Normal Mitotic
10 uM
1 uM
100 nM
10 nM
1 nM
0.1 nM
Concentration Taxol

Fig. 5

Scatter Plot

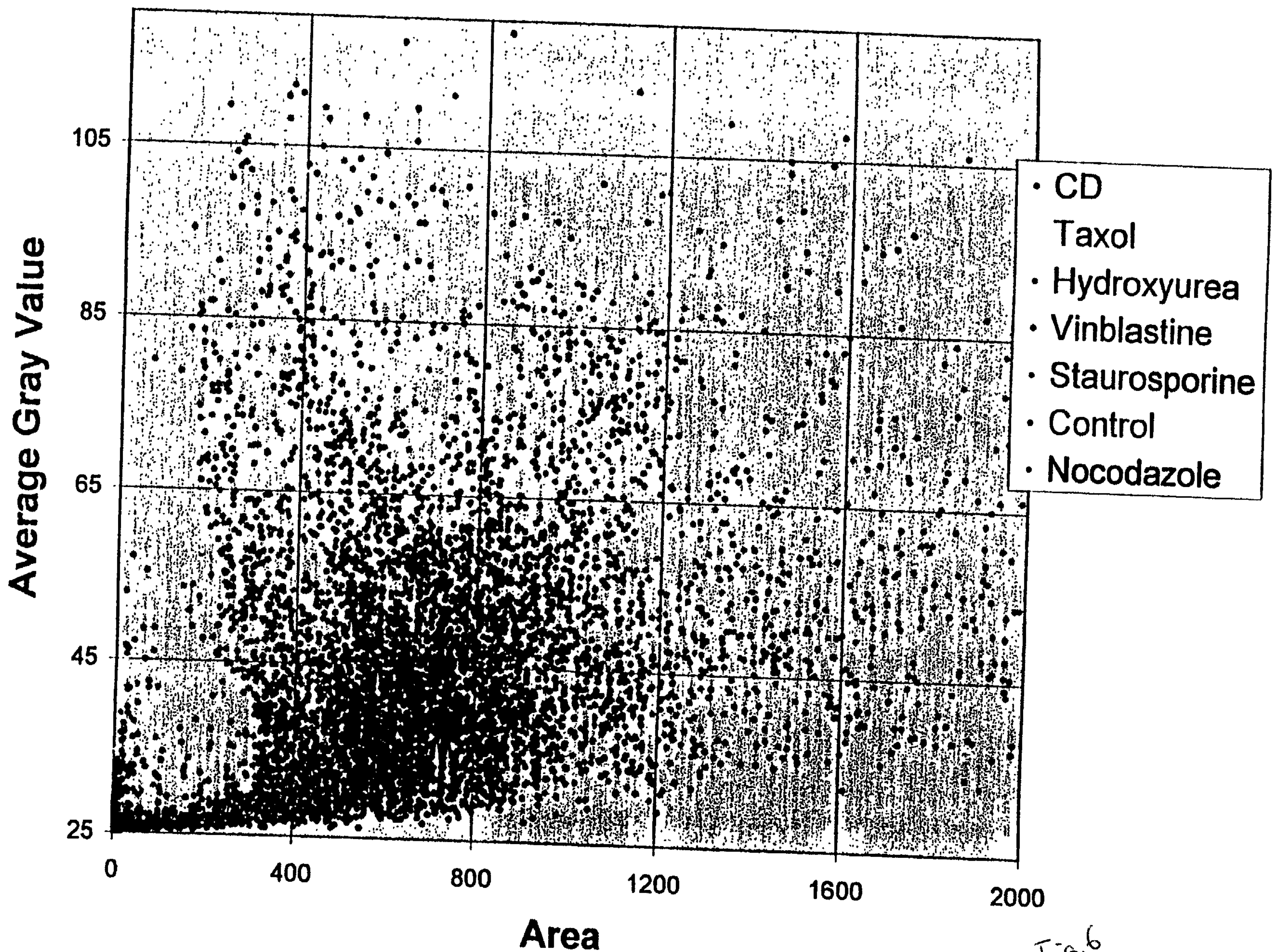


Fig. 6

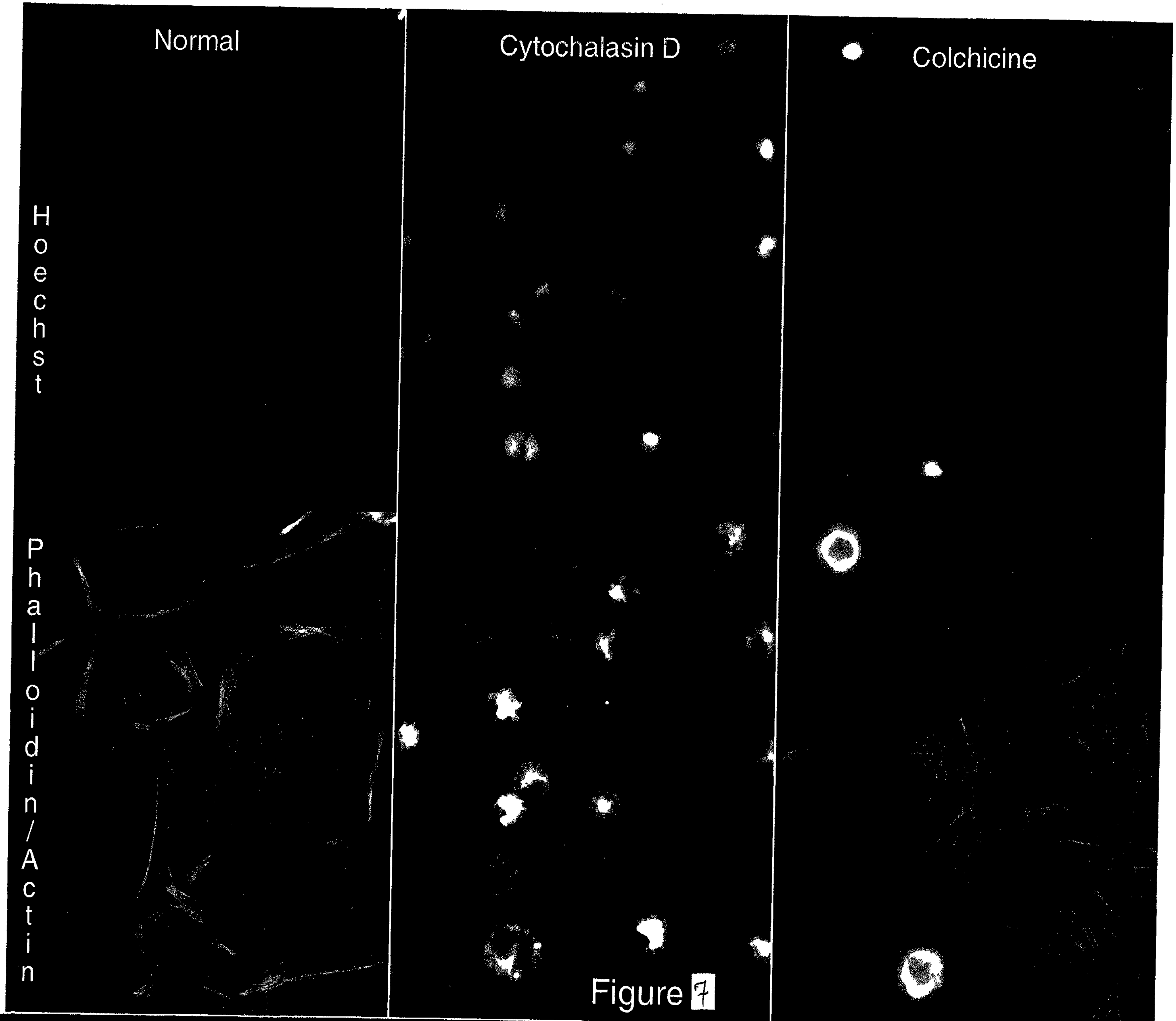

Normal
Cytochalasin D
Colchicine
Hoechst
Phalloidin/Actin

Figure 7

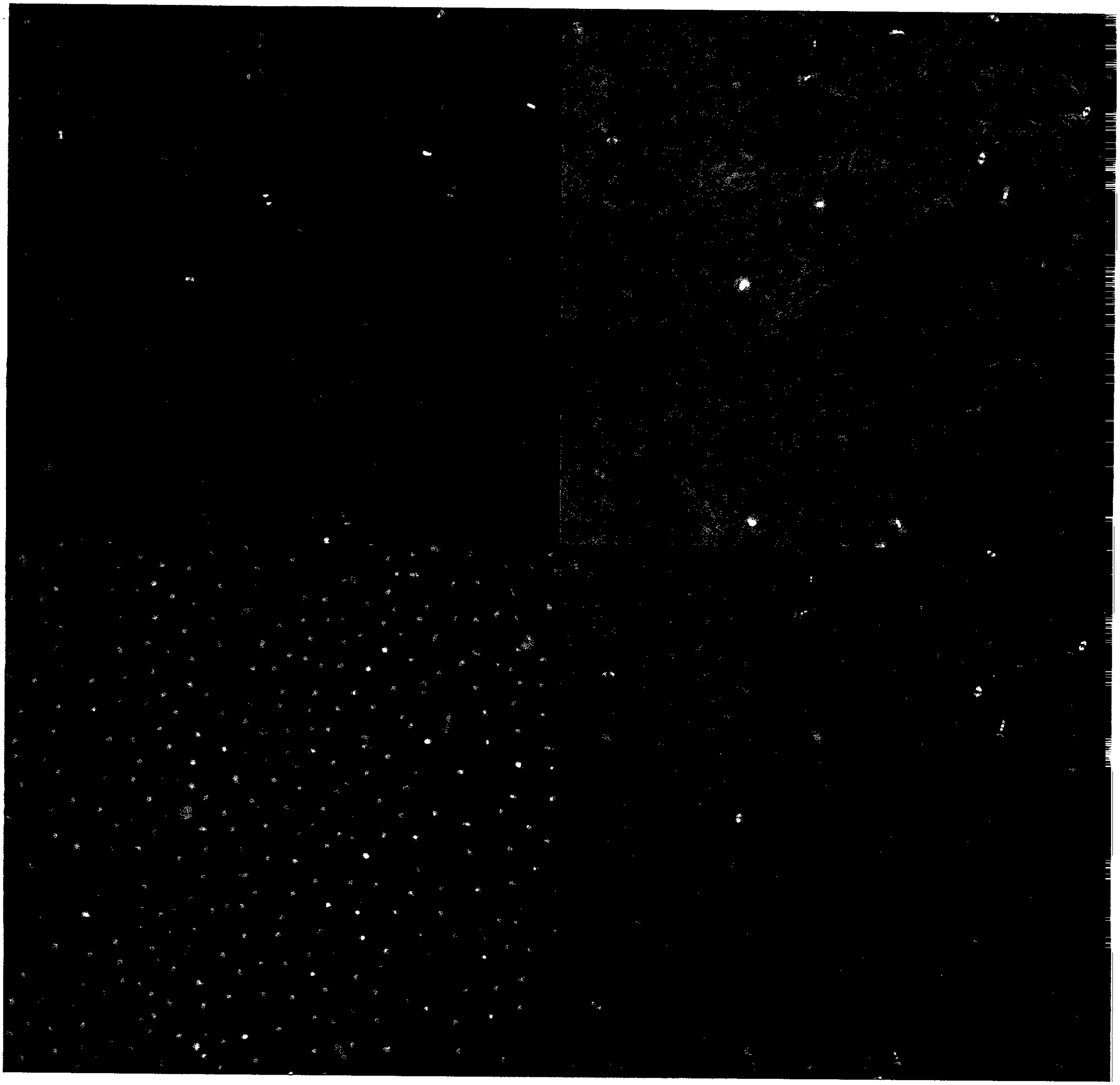


FIG. 8

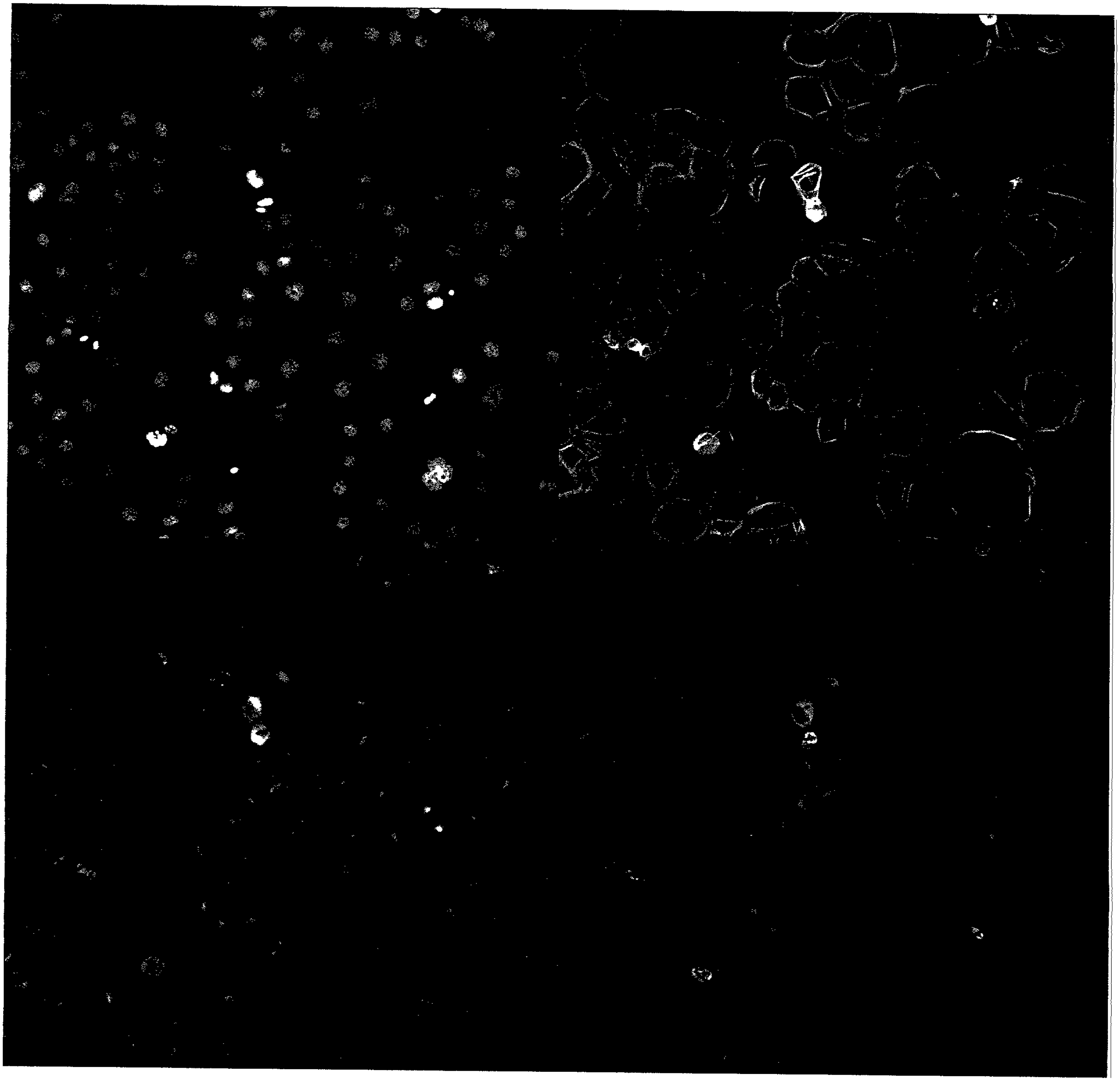


FIG.9

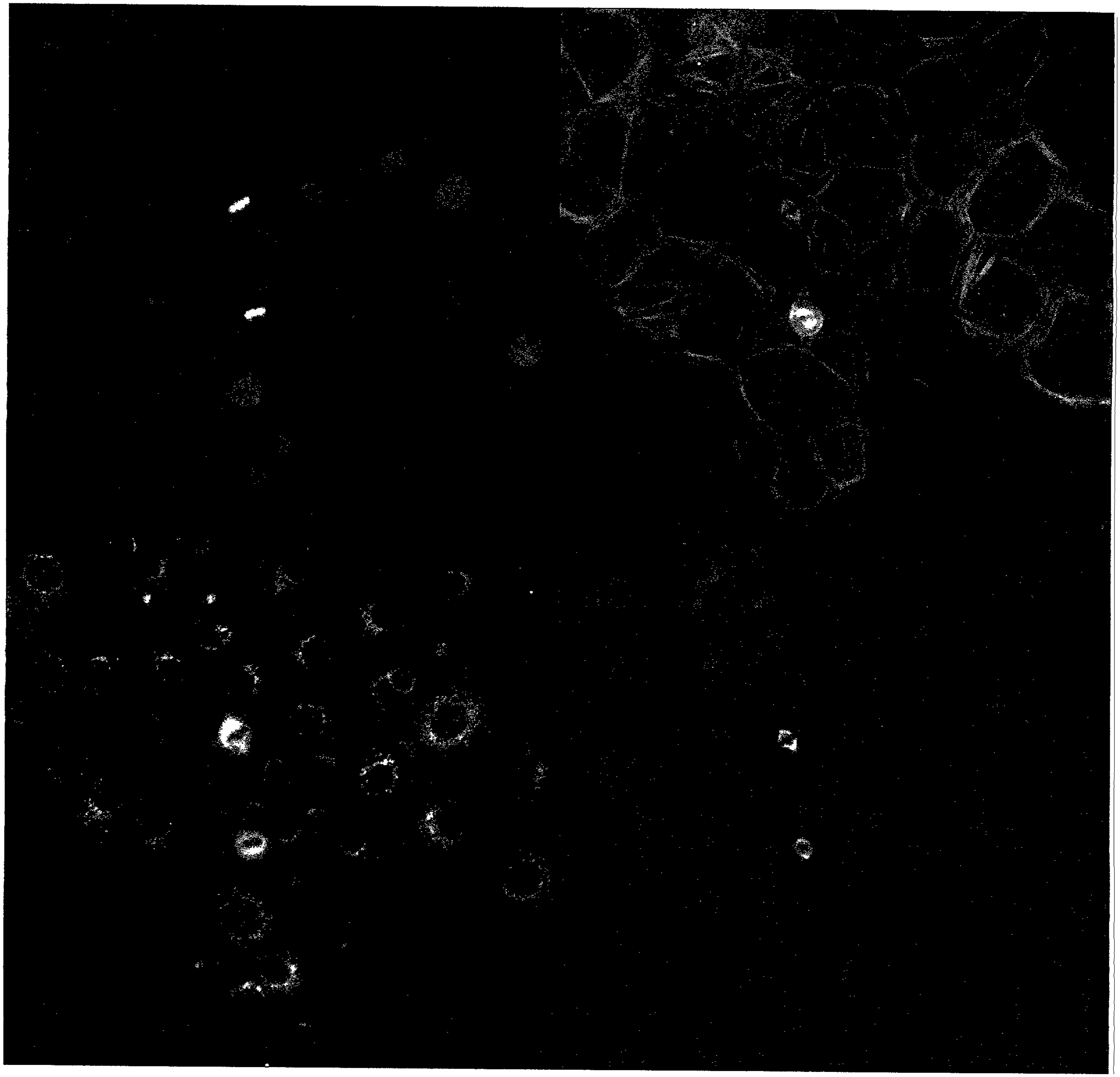


FIG. 10

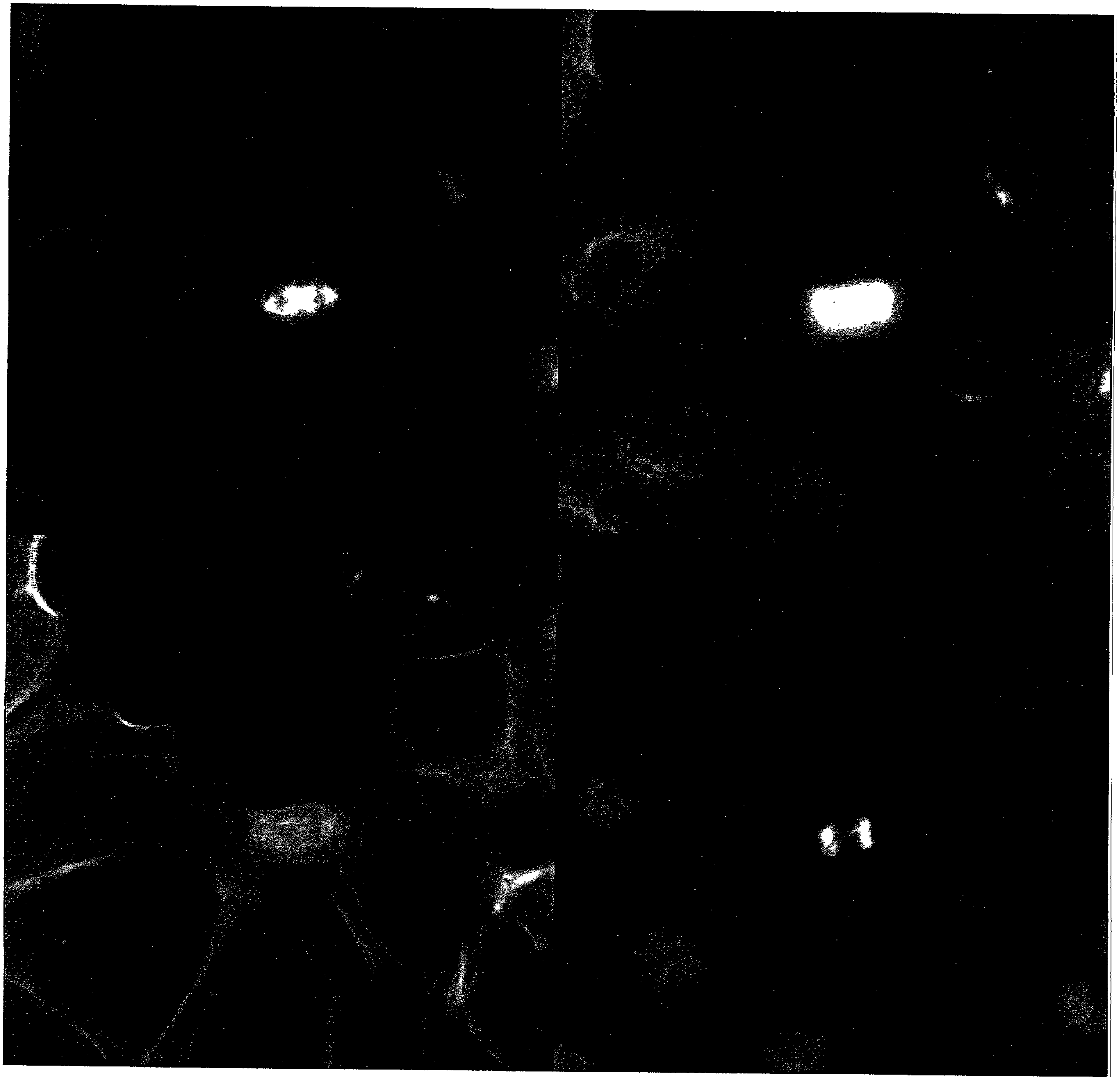


FIG. 11

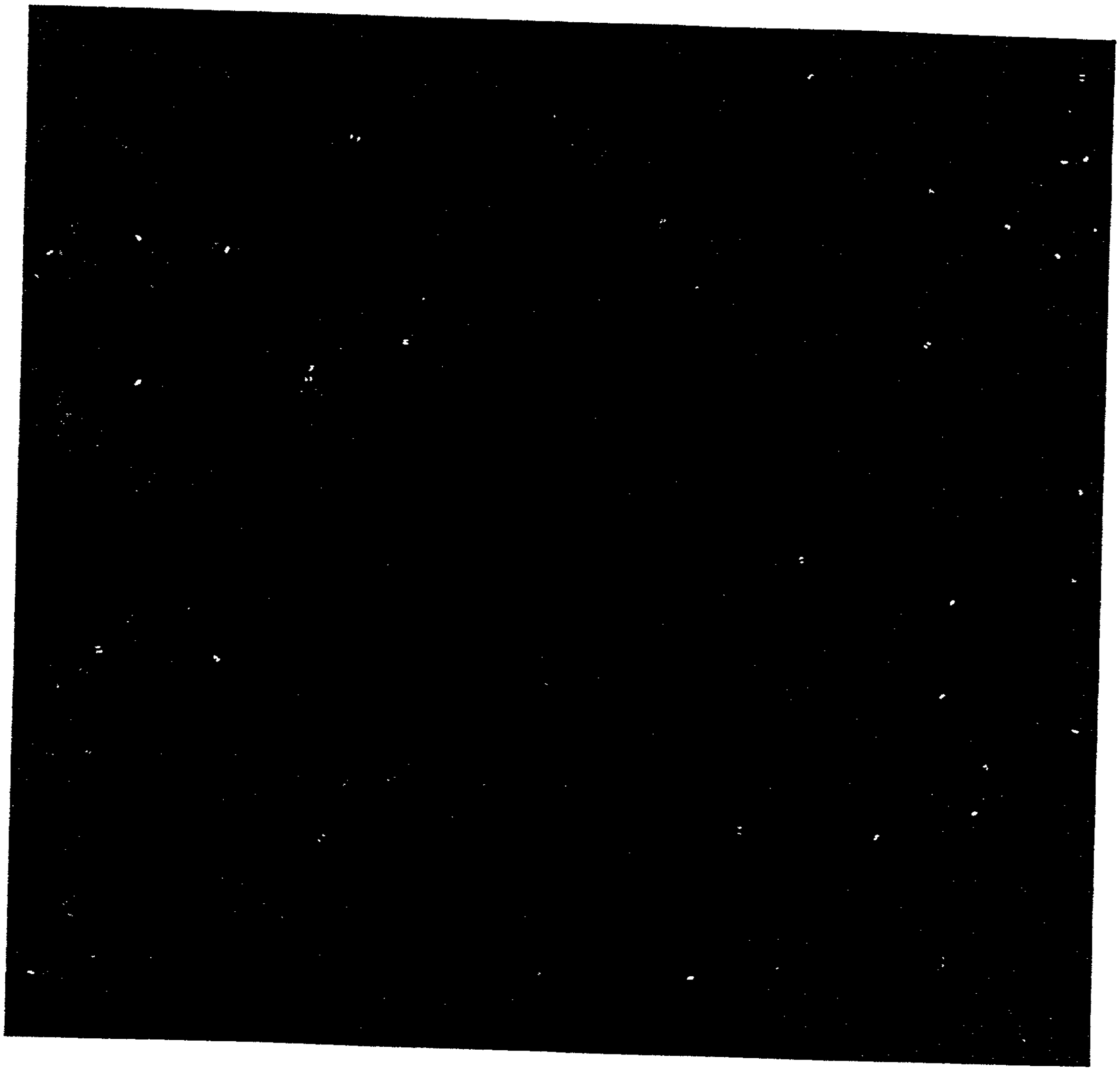


FIG 12

Conversion of morphometric parameters into nucleic acid code and clustering of the resulting sequences using Neighbor Joining method.

Compound:	Count	Area	Perimeter	Length	Breadth	Fiber length	Fiber breadth	Shape factor	Ell. form factor	Inner radius	Outer radius	Mean radius	Equiv. radius	Equiv. sphere vol.	Equiv. prolate vol.	Equiv. oblate vol.	Equiv. sphere surface area	Average gray value	Total gray value	Optical density	Radial dispersion	Texture Difference Moment	EFA Harmonic 2, Semi-Maj	EFA Harmonic 2, Semi-Min
Control	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	a	t	t
Taxol	a	t	t	t	t	t	t	t	a	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t
CD	c	a	a	a	t	a	t	t	c	a	a	a	a	a	a	a	a	t	a	a	a	t	a	g
Nocodozol	c	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t
Staurosporine	g	g	c	a	a	t	a	a	t	g	a	a	a	t	g	g	g	a	a	t	a	t	a	a
Vinblastine	c	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	t	g	t	t	t	t	t
Hydroxyurea	g	t	t	t	t	t	t	g	t	t	t	t	t	t	t	t	t	t	t	c	t	a	t	t

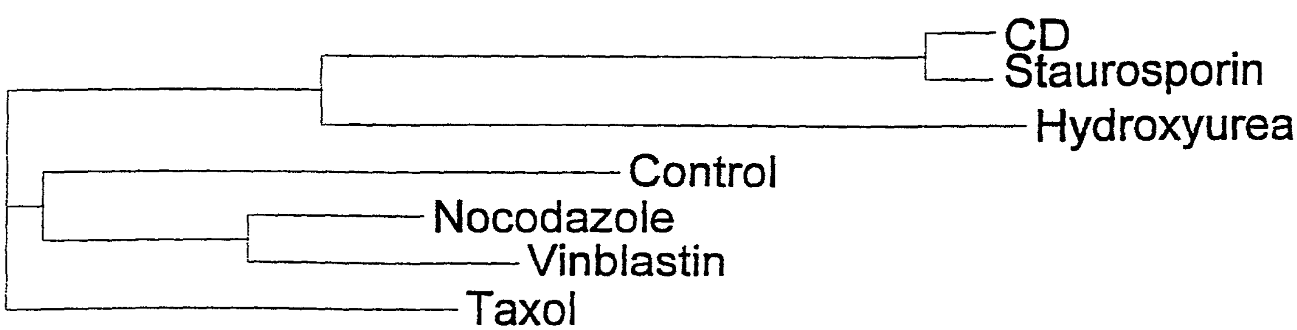


FIG 13

Conversion of morphometric parameters into amino acid codes and clustering of the resulting sequences using Neighbor Joining method.

	Count	Area	Perimeter	Length	Breadth	Fiber length	Fiber breadth	Shape factor	Ell. form factor	Inner radius	Outer radius	Mean radius	Equiv. radius	Equiv. sphere vol.	Equiv. prolate vol.	Equiv. oblate vol.	Equiv. sphere surface a	Average gray value	Total gray value	Optical density	Radial dispersion	Texture Difference Mo	EFA Harmonic 2, Semi-	EFA Harmonic 2, Semi-	
Control	H	P	T	T	N	S	D	W	E	S	T	T	T	F	C	C	P	P	M	C	T	G	T	T	Y
Taxol	G	F	M	M	P	M	P	H	G	S	M	M	W	C	F	P	F	R	C	M	M	H	M	P	S
CD	F	G	G	G	M	G	M	K	A	G	G	G	G	G	G	G	G	H	G	G	G	M	G	V	H
Nocodozol	W	F	M	M	W	M	P	T	R	S	M	M	M	F	M	W	F	M	M	R	M	M	M	F	G
Staurosporine	N	V	A	G	G	M	G	G	Y	V	G	G	G	M	V	V	V	G	G	H	G	M	G	G	V
Vinblastine	F	W	W	M	W	W	C	W	D	S	M	W	W	M	M	M	W	M	V	E	M	M	M	F	P
Hydroxyurea	S	H	H	H	H	H	H	V	H	H	H	H	H	H	H	H	H	H	H	A	H	G	H	H	D

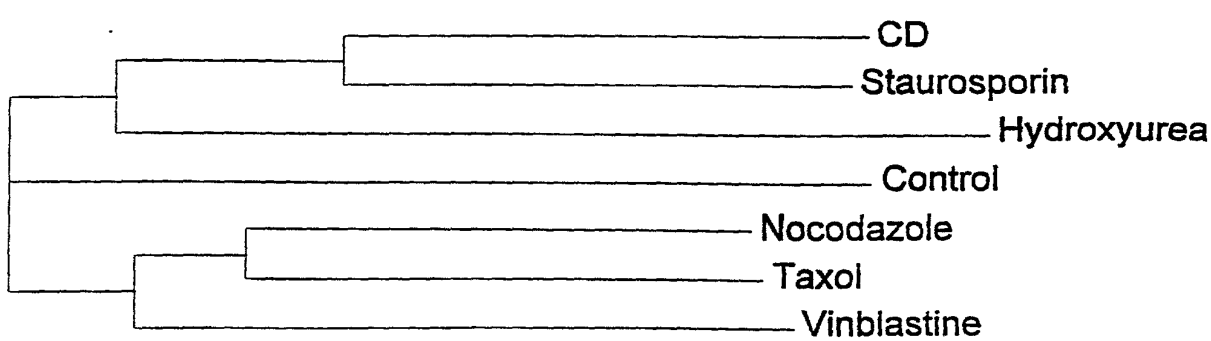


FIG 14

Attorney Docket No.: 19681-4

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I declare that:

My residence, post office address and citizenship are as stated below next to my name; I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: **A DATABASE SYSTEM INCLUDING COMPUTER CODE FOR PREDICTIVE CELLULAR BIOINFORMATICS** the specification of which _X_ is attached hereto or ___ was filed on __________ as Application No. __________ and was amended on __________ (if applicable).

I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56. I claim foreign priority benefits under Title 35, United States Code, Section 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Country	Application No.	Date of Filing	Priority Claimed Under 35 USC 119

I claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

Application No.	Date of Filing	Status

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Paul A. Durdik, Reg. No. 37,819
Karen Dow, Reg. No. 29,684
Richard T. Ogawa, Reg. No. 37,692

Send Correspondence to:	Direct Telephone Calls to:
Paul A. Durdik	(Name, Reg. No., Telephone No.)
TOWNSEND and TOWNSEND and CREW LLP	Name: Paul A. Durdik
Two Embarcadero Center, 8th Floor	Reg. No.: 37,819
San Francisco, California 94111-3834	Telephone: 650-326-2400

Full Name of Inventor 1:	Last Name: VAISBERG	First Name: EUGENI	Middle Name or Initial: A.	
Residence & Citizenship:	City: Foster City	State/Foreign Country: California	Country of Citizenship: Russian Federation	
Post Office Address:	Post Office Address: 647 Pegasus Lane	City: Foster City	State/Country: California	Postal Code: 94404

Attorney Docket No.: 19681-4

Full Name of Inventor 2:	Last Name: ADAMS	First Name: CYNTHIA	Middle Name or Initial: L.	
Residence & Citizenship:	City: Palo Alto	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 615 Georgia Avenue	City: Palo Alto	State/Country: California	Postal Code: 94306
Full Name of Inventor 3:	Last Name: SABRY	First Name: JAMES	Middle Name or Initial: H.	
Residence & Citizenship:	City: San Francisco	State/Foreign Country: California	Country of Citizenship: Canada	
Post Office Address:	Post Office Address: 4305 20th Street	City: San Francisco	State/Country: California	Postal Code: 94114
Full Name of Inventor 4:	Last Name: CROMPTON	First Name: ANNE	Middle Name or Initial: M.	
Residence & Citizenship:	City: San Francisco	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 2 Bellair Place	City: San Francisco	State/Country: California	Postal Code: 94133

further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Signature of Inventor 1	Signature of Inventor 2	Signature of Inventor 3
EUGENI A. VAISBERG	CYNTHIA L. ADAMS	JAMES H. SABRY
Date 5-13-99	Date 051399	Date 5-13-99

Signature of Inventor 4
ANNE M. CROMPTON
Date 5-13-99

SCANNED, # 9

PA 191459 v1

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Application No.: NEW

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Title: DATABASE SYSTEM INCLUDING COMPUTER FOR PREDICTIVE CELLULAR BIOINFORMATICS

ASSOCIATE POWER OF ATTORNEY AND CHANGE OF CORRESPONDENCE ADDRESS IN APPLICATION

Assistant Commissioner for Patents
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Sir:

The undersigned attorney of record in the subject patent application hereby grants an Associate Power of Attorney to add the law firm of Beyer Weaver & Thomas, LLP and all practitioners who are associated with the **Customer Number 022434** to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Respectfully submitted,
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Date: November 21, 2000

APPENDIX A

Example of the output of AnalyseDNA.m program
(measurements for a single 3 by 3 montage image)

File#	Subimage	object#	X coord	Y coord	Area	Axes ratio	Eccentri-sity	EquvDiam	Solidity	Extent	Intensi-ty	Avg. intens	median intens.	20% pix.	80% pix
1	1	1	12.2897	152.655	145	1.17293	0.522624	13.5875	0.923567	0.739796	4605	31.7586	34	25	37
0															
1	1	2	16.352	416.032	125	1.60594	0.782471	12.6157	0.905797	0.78125	4606	36.848	38	30	45
1	1	3	20.1073	73.8079	177	1.09845	0.413785	15.0121	0.917098	0.691406	4769	26.9435	29	22	31
1	1	4	21.4186	402.744	43	1.36215	0.679004	7.39928	0.914894	0.767857	3690	85.814	87	67	105
1	1	5	27.0938	184	96	1.30887	0.645194	11.0558	0.888889	0.671329	4502	46.8958	49	38	56
1	1	6	30.3252	259.534	206	2.33106	0.903309	16.1953	0.927928	0.715278	6380	30.9709	33	24	37
1	1	7	33.6629	167.573	89	1.34984	0.671696	10.6451	0.927083	0.741667	4225	47.4719	50	39	56
1	1	8	35.0411	16.9726	146	1.25176	0.601495	13.6343	0.929936	0.748718	5415	37.089	40	29	44
1	1	9	37.766	366.021	47	1.84062	0.839542	7.73578	0.87037	0.652778	6667	141.851	142	113	171
1	1	10	49.1078	170.004	232	1.90491	0.851127	17.187	0.852941	0.70303	9832	42.3793	45	33	51
1	1	11	56.0769	126.534	221	1.95704	0.859595	16.7746	0.924686	0.686335	7040	31.8552	33	25	37
1	1	12	52.7755	44.9932	147	1.33627	0.663301	13.6809	0.907407	0.706731	4765	32.415	34	26	39
1	1	13	52.4444	366.854	171	2.27225	0.897953	14.7555	0.872449	0.706612	9378	54.8421	56	43	68
1	1	14	56.4029	282.272	206	1.92782	0.854944	16.1953	0.923767	0.64375	7137	34.6456	37	28	41
1	1	15	57.0648	227.176	108	1.73885	0.818089	11.7265	0.915254	0.701299	4644	43	45	33	51
1	1	16	68.1714	333.181	315	1.11194	0.437266	20.0267	0.75	0.526756	15151	48.0984	50	36	62
1	1	17	65.1409	402.414	220	1.70147	0.80906	16.7366	0.920502	0.647059	9809	44.5864	46	35	54
1	1	18	71.8649	443.13	185	1.77678	0.826583	15.3476	0.91133	0.649123	6124	33.1027	35	25	39
1	1	19	73.626	184.854	123	1.71588	0.812622	12.5143	0.911111	0.723529	4841	39.3577	41	30	47
1	1	20	77.4869	132.513	306	1.6379	0.791988	19.7386	0.822581	0.632231	14559	47.5784	50	38	57
1	1	21	78.7377	208.27	122	1.3357	0.662941	12.4634	0.910448	0.739394	4483	36.7459	40	29	43
1	1	22	81.4786	53.5812	117	1.64713	0.794614	12.2053	0.886364	0.642857	4686	40.0513	43	32	47
1	1	23	88.7292	281.534	373	2.17388	0.887916	21.7926	0.843891	0.531339	16109	43.1877	46	34	52
1	1	24	84.1765	341.976	85	1.20799	0.560991	10.4031	0.876289	0.708333	4589	53.9882	57	43	63
1	1	25	88.1608	176.231	143	1.43573	0.717545	13.4935	0.940789	0.794444	4878	34.1119	35	27	41
1	1	26	91.4529	376.924	170	1.36853	0.682689	14.7123	0.949721	0.833333	4933	29.0176	30	23	35
1	1	27	97.7604	317.795	288	1.97353	0.862119	19.1492	0.9	0.606316	10663	37.0243	39	29	45
1	1	28	96.5841	230.363	113	1.09835	0.413609	11.9948	0.896825	0.668639	4540	40.177	43	33	48
1	1	29	96.9492	248.602	118	1.2774	0.622219	12.2573	0.921875	0.766234	4873	41.2966	43	32	51
1	1	30	103.033	93.3279	122	1.48415	0.738927	12.4634	0.945736	0.813333	4663	38.2213	40	31	47
1	1	31	103.47	155.507	134	1.5208	0.753411	13.0619	0.917808	0.687179	4358	32.5224	34	27	38
1	1	32	105.356	57.1271	118	1.90339	0.850869	12.2573	0.907692	0.694118	4695	39.7881	42	30	49
1	1	33	121.23	285.08	326	1.70329	0.809514	20.3734	0.900552	0.626923	15864	48.6626	50	39	60
1	1	34	125.532	170.645	141	1.53045	0.757011	13.3988	0.927632	0.734375	6429	45.5957	49	37	53
1	1	35	128.98	60.3355	152	1.75689	0.822208	13.9116	0.921212	0.767677	6875	45.2303	47	36	54
1	1	36	137.083	128.083	266	1.845	0.840375	18.4033	0.796407	0.538462	9810	36.8797	38	26	45
1	1	37	130.902	411.5	164	1.19276	0.54507	14.4503	0.937143	0.788462	7337	44.7378	47	35	53
1	1	38	132.439	352.545	187	1.39705	0.698312	15.4304	0.935	0.799145	5227	27.9519	27	22	34
1	1	39	129.615	16.6154	13	1.15921	0.50579	4.06843	0.928571	0.8125	94	7.23077	8	3	11
1	1	40	136.574	209.099	101	1.12013	0.450546	11.3401	0.87069	0.647436	7293	72.2079	74	58	88
1	1	41	134.455	33.0909	33	1.21149	0.564506	6.48204	0.916667	0.785714	1949	59.0606	60	44	75
1	1	42	140.893	102.008	121	1.47787	0.736306	12.4122	0.916667	0.733333	4808	39.7355	40	32	47
1	1	43	144.864	59.8199	272	1.75519	0.821825	18.6097	0.934708	0.725333	10814	39.7574	41	32	48
1	1	44	147.093	438.435	161	1.3071	0.64397	14.3175	0.925287	0.715556	9000	55.9006	58	44	68
1	1	45	151.46	256.924	224	1.08008	0.377872	16.888	0.937238	0.777778	9654	43.0982	45	33	53
1	1	46	155.688	178.546	141	1.39135	0.695293	13.3988	0.921569	0.801136	7729	54.8156	57	44	65
1	1	47	160.875	342.354	48	1.71551	0.812532	7.81764	0.857143	0.592593	6609	137.688	139	103	168
1	1	48	168.828	11.7677	198	1.42126	0.710595	15.8777	0.933962	0.733333	9931	50.1566	50	39	62
1	1	49	169.613	136.267	217	1.74718	0.820008	16.6221	0.825095	0.5425	7980	36.7742	38	28	45
1	1	50	176.014	356.414	222	1.44188	0.720419	16.8125	0.790036	0.621849	9626	43.3604	46	33	54
1	1	51	175.788	192.983	118	1.13784	0.47708	12.2573	0.900763	0.698225	4671	39.5847	42	32	47
1	1	52	177.181	210.874	127	1.14539	0.487604	12.7162	0.92029	0.755952	4862	38.2835	40	30	45
1	1	53	178.367	410.524	147	1.24127	0.592425	13.6809	0.924528	0.75	9096	61.8776	67	50	72
1	1	54	182.4	392.476	170	1.52768	0.755987	14.7123	0.939227	0.714286	9335	54.9118	58	44	66
1	1	55	189.388	262.719	196	1.81704	0.834936	15.7973	0.915888	0.742424	5030	25.6633	27	20	31
1	1	56	200.742	93.7418	213	1.36983	0.683428	16.4682	0.934211	0.747368	9665	45.3756	48	38	53
1	1	57	199.198	156.725	91	1.04663	0.295161	10.7641	0.90099	0.752066	4188	46.022	47	36	56
1	1	58	209.67	185.871	264	1.96083	0.860182	18.334	0.916667	0.6	9873	37.3977	39	29	46
1	1	59	208.752	70.0435	230	1.69129	0.806478	17.1127	0.946502	0.804196	9766	42.4609	44	34	53
1	1	60	212.584	368.695	197	1.13679	0.475587	15.8376	0.929245	0.724265	7014	35.6041	36	27	44
1	1	61	220.856	30.6237	194	2.67662	0.927588	15.7165	0.92823	0.776	4635	23.8918	25	18	29
1	1	62	216.568	234.29	183	1.34183	0.666785	15.2644	0.943299	0.828054	5078	27.7486	28	21	34
1	1	63	216.292	293.953	171	1.64627	0.79437	14.7555	0.919355	0.692308	5053	29.5497	30	23	35
1	1	64	217.331	330.721	172	1.72537	0.81491	14.7986	0.924731	0.671875	5040	29.3023	31	22	36
1	1	65	217.388	427.1	201	1.29372	0.634448	15.9975	0.926267	0.738971	6094	30.3184	32	25	36
1	1	66	222.926	157.769	121	1.3261	0.656767	12.4122	0.916667	0.733333	4352	35.9669	38	29	42
1	1	67	249.071	488.968	435	3.20117	0.949955	23.5342	0.74359	0.402778	14810	34.046	37	26	42
1	1	68	238.844	265.186	167	1.48408	0.738897	14.5819	0.938202	0.755656	5158	30.8862	32	25	37

1	1	69	243.509	88.7857	224	1.87991	0.846782	16.888	0.899598	0.636364	8827	39.4063	42	30	49
1	1	70	248.831	322.144	160	1.79681	0.830819	14.273	0.91954	0.76555	5025	31.4063	33	25	38
1	1	71	249.234	413.026	77	1.15366	0.498651	9.90149	0.875	0.7	4352	56.5195	59	46	67
1	1	72	256.945	43.816	163	1.58857	0.777002	14.4062	0.91573	0.679167	4720	28.9571	30	23	34
1	1	73	257.061	398.848	66	1.03149	0.245208	9.167	0.916667	0.814815	4440	67.2727	71	56	80
1	1	74	263.602	375.59	251	1.95991	0.860039	17.8769	0.886926	0.597619	10500	41.8327	43	32	50
1	1	75	264.292	233.801	161	1.65084	0.795652	14.3175	0.914773	0.688034	5136	31.9006	33	25	38
1	1	76	264.937	209.802	111	1.31512	0.649472	11.8882	0.917355	0.720779	4858	43.7658	45	36	52
1	1	77	266.137	348.328	131	1.58185	0.774829	12.9149	0.909722	0.682292	9633	73.5344	77	56	89
1	1	78	276.221	171.24	204	2.05613	0.873763	16.1165	0.918919	0.596491	7051	34.5637	35	28	41
1	1	79	277.059	285.098	287	1.27833	0.622935	19.116	0.87234	0.650794	10520	36.6551	38	29	45
1	1	80	278.327	97.32	150	1.10321	0.422329	13.8198	0.920245	0.765306	9202	61.3467	63	42	78
1	1	81	276.612	391.118	85	1.67318	0.801747	10.4031	0.923913	0.817308	4387	51.6118	55	43	62
1	1	82	285.905	154.719	231	1.56301	0.76855	17.1499	0.931452	0.675439	8580	37.1429	39	31	44
1	1	83	285.326	203.688	221	1.75638	0.822092	16.7746	0.863281	0.701587	10251	46.3846	49	34	57
1	1	84	284.739	355.022	46	1.74017	0.818394	7.65304	0.867925	0.730159	6986	151.87	159	120	185
1	1	85	291.4	319.71	145	1.31364	0.648467	13.5875	0.917722	0.755208	4940	34.069	35	27	42
1	1	86	297.651	442.734	192	2.01531	0.868208	15.6353	0.941176	0.793388	5972	31.1042	32	23	39
1	1	87	293.81	389.276	58	1.25774	0.60651	8.59348	0.920635	0.725	3964	68.3448	70	55	82
1	1	88	299.182	285.182	159	1.39289	0.696112	14.2283	0.929825	0.757143	5103	32.0943	33	26	39
1	1	89	300.14	356.347	150	1.31538	0.649643	13.8198	0.925926	0.78125	5369	35.7933	37	30	41
1	1	90	311.5	260.38	382	1.57517	0.772632	22.054	0.843267	0.598746	16117	42.1911	44	32	53
1	1	91	308.77	132.894	161	1.15063	0.49465	14.3175	0.936047	0.766667	4966	30.8447	33	24	38
1	1	92	312.161	21.8111	180	1.62866	0.789304	15.1388	0.932642	0.728745	4915	27.3056	28	22	32
1	1	93	308.683	204.548	126	1.6436	0.793615	12.666	0.9	0.7	4950	39.2857	40	31	48
1	1	94	317.72	43.06	150	2.18043	0.88863	13.8198	0.882353	0.595238	4958	33.0533	35	25	41
1	1	95	315.779	222.448	145	1.2166	0.569542	13.5875	0.917722	0.74359	5048	34.8138	36	28	42
1	1	96	314.612	396.048	147	1.78365	0.828055	13.6809	0.936306	0.773684	9195	62.551	65	47	78
1	1	97	319.321	79.6831	243	1.37849	0.688296	17.5897	0.945525	0.759375	8192	33.7119	36	27	39
1	1	98	327.995	171.85	207	1.17294	0.52263	16.2345	0.928251	0.761029	4993	24.1208	25	19	29
1	1	99	327.232	313.626	99	1.27961	0.623918	11.2272	0.933962	0.761538	4632	46.7879	50	35	57
1	1	100	328.895	465.333	153	1.61993	0.786719	13.9573	0.9	0.6375	4428	28.9412	30	22	36
1	1	101	339.875	30.4024	328	2.08757	0.877801	20.4358	0.896175	0.594203	10208	31.122	33	24	38
1	1	102	336.286	341.101	168	1.36659	0.681577	14.6255	0.928177	0.746667	4848	28.8571	29	23	35
1	1	103	335.277	126.088	137	1.47067	0.733247	13.2073	0.901316	0.713542	6932	50.5985	53	41	59
1	1	104	336.608	376.692	130	1.44662	0.722601	12.8655	0.902778	0.666667	4713	36.2538	38	29	43
1	1	105	340.273	422.859	128	1.82797	0.837097	12.7662	0.920863	0.65641	4609	36.0078	38	29	43
1	1	106	341.624	392.101	149	1.21343	0.566431	13.7736	0.925466	0.764103	4920	33.0201	35	27	38
1	1	107	353.93	211.249	201	1.50656	0.747942	15.9975	0.922018	0.773077	8487	42.2239	43	34	51
1	1	108	352.982	107.865	170	1.49726	0.744263	14.7123	0.909091	0.688259	4955	29.1471	30	23	36
1	1	109	360.316	246.868	152	1.86075	0.843317	13.9116	0.894118	0.596078	5109	33.6118	35	25	41
1	1	110	357.882	436.327	110	1.20428	0.557215	11.8345	0.901639	0.714286	4290	39	41	30	48
1	1	111	361.836	318.483	116	1.51165	0.749922	12.153	0.885496	0.644444	4620	39.8276	42	32	48
1	1	112	361.357	65	140	1.27314	0.618912	13.3512	0.933333	0.777778	4854	34.6714	35	27	43
1	1	113	363.058	282.398	103	1.26774	0.614641	11.4518	0.927928	0.792308	4724	45.8641	47	36	56
1	1	114	377.556	52.6893	383	2.24284	0.895101	22.0828	0.851111	0.526099	12083	31.5483	30	23	44
1	1	115	369.901	346.09	111	1.32541	0.656322	11.8882	0.909836	0.776224	4428	39.8919	41	31	48
1	1	116	372.355	389.158	183	1.08717	0.392338	15.2644	0.953125	0.871429	4673	25.5355	26	19	32
1	1	117	375.494	102.31	168	1.77626	0.82647	14.6255	0.913043	0.658824	6590	39.2262	41	32	48
1	1	118	377.238	164.669	172	1.55567	0.766024	14.7986	0.910053	0.67451	5008	29.1163	30	24	35
1	1	119	378.105	487.237	190	1.34387	0.668045	15.5536	0.913462	0.698529	6078	31.9895	32	23	41
1	1	120	386.803	129.803	142	1.82726	0.836959	13.4462	0.940397	0.788889	8149	57.3873	61	48	69
1	1	121	387.01	222.932	206	1.51589	0.751547	16.1953	0.923767	0.792308	10014	48.6117	50	37	60
1	1	122	384.354	305.719	96	1.74508	0.819527	11.0558	0.923077	0.666667	4564	47.5417	48	36	59
1	1	123	397.856	400.719	313	1.71338	0.812011	19.9631	0.800512	0.610136	14036	44.8435	46	36	56
1	1	124	389.741	281.944	108	1.86676	0.844417	11.7265	0.892562	0.593407	4668	43.2222	44	33	53
1	1	125	393.248	318.762	105	1.49331	0.742673	11.5624	0.913043	0.673077	4613	43.9333	46	36	52
1	1	126	395.708	20.375	120	1.06484	0.34362	12.3608	0.916031	0.769231	4538	37.8167	39	32	45
1	1	127	402.593	198.495	194	1.83729	0.838903	15.7165	0.932692	0.769841	9702	50.0103	52	39	61
1	1	128	403.562	362.046	130	2.18482	0.889105	12.8655	0.902778	0.601852	4566	35.1231	37	28	43
1	1	129	402.298	35.0744	121	1.34169	0.666695	12.4122	0.909774	0.720238	4622	38.1983	41	31	45
1	1	130	407.174	349.358	109	1.26316	0.610958	11.7806	0.908333	0.698718	4433	40.6697	42	31	49
1	1	131	410.641	432.387	142	2.10237	0.879632	13.4462	0.898734	0.71	4284	30.169	32	23	37
1	1	132	408.948	170.017	174	1.43507	0.717235	14.8843	0.910995	0.74359	4845	27.8448	29	21	35
1	1	133	415.673	271.184	147	1.36843	0.682628	13.6809	0.93038	0.765625	4976	33.8503	36	28	39
1	1	134	419.881	320.856	118	1.70261	0.809346	12.2573	0.887218	0.605128	4596	38.9492	41	31	48
1	1	135	428.797	224.645	172	1.24283	0.593793	14.7986	0.92973	0.764444	5120	29.7674	32	24	35
1	1	136	428.437	38.3016	126	1.24199	0.593057	12.666	0.926471	0.75	4585	36.3889	39	30	43
1	1	137	434.977	106.932	222	1.74232	0.818891	16.8125	0.925	0.720779	7043	31.7252	33	25	38
1	1	138	432.809	424.282	131	1.70121	0.808993	12.9149	0.922535	0.770588	4251	32.4504	33	24	40
1	1	139	431.155	477.519	129	1.14151	0.48225	12.8159	0.914894	0.767857	4387	34.0078	35	27	41
1	1	140	438.675	12.7222	126	1.27999	0.624207	12.666	0.933333	0.75	4445	35.2778	38	26	42
1	1	141	441.29	464.766	124	1.33453	0.662198	12.5651	0.918519	0.688889	4658	37.5645	40	30	45
1	1	142	445.287	152.375	136	1.38301	0.690787	13.159	0.912752	0.708333	5017	36.8897	39	28	44
1	1	143	452.32	495.598	306	1.66314	0.799045	19.7386	0.918919	0.796875	17726	57.9281	61	47	68
1	1	144	451.122	370.49	288	1.77678	0.826582	19.1492	0.825215	0.659039	11388	39.5417	42	30	49

1	1	145	462.718	316.942	291	2.5992	0.923028	19.2487	0.716749	0.534926	9565	32.8694	32	23	43
1	1	146	455.84	345.437	119	1.51711	0.752012	12.3092	0.915385	0.793333	4473	37.5882	39	28	46
1	1	147	459.357	398.325	154	1.73345	0.816825	14.0028	0.922156	0.712963	8038	52.1948	55	42	62
1	1	148	459.428	30.199	201	1.48473	0.739168	15.9975	0.934884	0.755639	4615	22.9602	24	18	27
1	1	149	462.472	163.039	127	1.2763	0.621371	12.7162	0.947761	0.824675	4849	38.1811	40	30	46
1	1	150	465.094	234.432	405	1.32102	0.653423	22.7082	0.89404	0.771429	9811	24.2247	25	19	29
1	1	151	459	185	23	1.22522	0.577796	5.41152	0.851852	0.657143	2687	116.826	118	86	135
1	1	152	469.289	73.6404	228	1.65352	0.796399	17.0382	0.919355	0.690909	8169	35.8289	37	28	44
1	1	153	468.291	365.573	117	1.37288	0.685157	12.2053	0.936	0.835714	4553	38.9145	40	32	45
1	1	154	469.261	188.174	23	1.17386	0.523719	5.41152	0.92	0.766667	2572	111.826	115	97	134
1	1	155	477.09	285.407	199	1.33807	0.664436	15.9177	0.947619	0.737037	7638	38.3819	40	31	46
1	1	156	480.109	124.384	138	1.47131	0.733523	13.2555	0.926174	0.704082	4514	32.7101	34	27	39
1	1	157	485.215	212.969	163	1.99846	0.865802	14.4062	0.91573	0.679167	6791	41.6626	43	33	51
1	1	158	493.535	460.984	129	1.46523	0.730898	12.8159	0.921429	0.716667	4590	35.5814	37	28	44
1	1	159	498.198	257.492	197	1.18457	0.536047	15.8376	0.933649	0.769531	6331	32.1371	34	25	38
1	1	160	498.107	428.713	122	1.39074	0.694967	12.4634	0.910448	0.739394	4778	39.1639	40	31	48
1	1	161	501.794	480.579	107	1.30083	0.639559	11.672	0.938596	0.743056	4301	40.1963	42	32	47
1	2	1	16.0133	189.207	150	1.82513	0.83654	13.8198	0.9375	0.789474	5013	33.42	35	26	40
1	2	2	13.3492	92.619	126	1.24511	0.595788	12.666	0.919708	0.75	4636	36.7937	39	31	44
1	2	3	12.7436	254.949	78	1.23696	0.588585	9.96557	0.906977	0.787879	4177	53.5513	54	42	65
1	2	4	21.4605	27.5132	152	2.05915	0.874161	13.9116	0.915663	0.59375	5398	35.5132	38	29	42
1	2	5	24.5889	412.717	180	1.41069	0.705337	15.1388	0.923077	0.714286	7613	42.2944	45	33	52
1	2	6	30.8013	150.013	151	1.5312	0.757285	13.8658	0.937888	0.807487	4834	32.0132	34	25	39
1	2	7	35.9216	117.641	153	1.10365	0.42309	13.9573	0.916168	0.728571	8847	57.8235	60	46	70
1	2	8	32.4386	483.965	57	1.17959	0.530388	8.51908	0.904762	0.791667	7839	137.526	142	104	175
1	2	9	41.1142	68.0551	254	2.15977	0.886352	17.9834	0.927007	0.575964	8532	33.5906	36	27	39
1	2	10	46.0943	205.164	159	1.43069	0.715156	14.2283	0.929825	0.779412	5043	31.717	32	25	38
1	2	11	47.0543	98.2403	129	1.6944	0.807273	12.8159	0.921429	0.661538	4858	37.6589	39	28	46
1	2	12	48.3986	164.971	138	1.40133	0.700548	13.2555	0.926174	0.784091	4896	35.4783	38	28	42
1	2	13	54.1071	128.629	140	1.31888	0.652002	13.3512	0.921053	0.777778	7556	53.9714	56	42	63
1	2	14	61.2347	252.877	375	1.46523	0.730898	21.851	0.868056	0.652174	18248	48.6613	52	38	60
1	2	15	58.7059	420.598	102	1.16735	0.515912	11.3961	0.902655	0.713287	8303	81.402	84	69	96
1	2	16	62.8217	461.434	286	1.44931	0.723823	19.0826	0.925566	0.654462	10326	36.1049	38	28	45
1	2	17	68.6289	183.686	194	1.89744	0.849849	15.7165	0.92823	0.769841	7275	37.5	39	29	47
1	2	18	72.3873	25.8873	204	1.65928	0.797991	16.1165	0.894737	0.647619	4906	24.049	26	18	29
1	2	19	83.1654	62.6808	260	1.92679	0.854775	18.1946	0.9319	0.656566	10031	38.5808	40	31	47
1	2	20	96.7188	481.695	256	2.0471	0.872567	18.0541	0.885813	0.592593	9587	37.4492	37	29	47
1	2	21	94.0154	108.485	130	1.50401	0.746944	12.8655	0.915493	0.738636	4616	35.5077	36	26	44
1	2	22	101.034	140.034	207	1.65907	0.797932	16.2345	0.924107	0.758242	9618	46.4638	48	37	56
1	2	23	106.469	179.984	254	2.25068	0.895873	17.9834	0.92029	0.552174	9484	37.3386	40	29	46
1	2	24	118.615	415.286	455	2.24916	0.895724	24.0692	0.803887	0.530303	19707	43.3121	45	31	56
1	2	25	109.325	462.783	157	1.33362	0.661618	14.1386	0.934524	0.769608	7940	50.5732	53	38	62
1	2	26	112.224	30.2115	156	1.68158	0.803963	14.0935	0.912281	0.65	4684	30.0256	31	24	37
1	2	27	114.738	94.3308	130	2.20139	0.89087	12.8655	0.866667	0.546218	4593	35.3308	36	27	45
1	2	28	113.664	117.473	131	1.89702	0.849777	12.9149	0.879195	0.582222	4551	34.7405	35	27	42
1	2	29	119.492	260.882	195	2.28309	0.898974	15.757	0.928571	0.633117	9042	46.3692	50	36	55
1	2	30	120.542	164.685	203	1.63181	0.790225	16.0769	0.931193	0.712281	9555	47.069	48	37	58
1	2	31	125.017	493.152	302	2.03965	0.871565	19.6091	0.92638	0.770408	16405	54.3212	57	43	66
1	2	32	128.12	375.544	125	1.54817	0.7634	12.6157	0.919118	0.686813	4694	37.552	39	29	46
1	2	33	134.357	246.786	182	1.30577	0.643043	15.2227	0.943005	0.764706	9424	51.7802	54	42	62
1	2	34	134.824	435.275	182	1.39127	0.69525	15.2227	0.933333	0.713725	9568	52.5714	55	42	63
1	2	35	137.463	477.361	205	1.67789	0.802993	16.1559	0.911111	0.719298	10137	49.4488	50	38	61
1	2	36	140.229	112.255	275	2.43852	0.912047	18.7121	0.813609	0.458333	9908	36.0291	38	27	45
1	2	37	144.759	62.396	303	2.77691	0.932909	19.6416	0.733656	0.510101	9815	32.3927	35	25	39
1	2	38	142.944	349.208	125	1.15101	0.495153	12.6157	0.925926	0.801282	4627	37.016	38	30	44
1	2	39	155.234	38.7854	410	2.62596	0.924652	22.8479	0.742754	0.415822	14441	35.222	36	25	47
1	2	40	145.827	141.547	150	1.38574	0.692274	13.8198	0.914634	0.721154	5019	33.46	35	26	40
1	2	41	171.118	418.674	144	2.13773	0.883842	13.5406	0.9	0.571429	4475	31.0764	32	24	38
1	2	42	169.885	483.963	218	2.03707	0.871215	16.6603	0.904564	0.619318	4735	21.7202	23	17	26
1	2	43	173.468	380.368	171	1.76541	0.824104	14.7555	0.909574	0.7125	4792	28.0234	30	21	34
1	2	44	173.139	451.197	122	1.71693	0.812877	12.4634	0.897059	0.717647	4270	35	34	27	44
1	2	45	177.184	127.971	343	2.17611	0.88816	20.8979	0.859649	0.714583	17821	51.9563	55	42	62
1	2	46	178.975	44.5574	122	1.47137	0.733547	12.4634	0.917293	0.739394	4501	36.8934	39	30	44
1	2	47	184.558	101.091	165	1.53097	0.757203	14.4943	0.921788	0.746606	5051	30.6121	32	25	36
1	2	48	187.282	274.494	174	2.03959	0.871557	14.8843	0.910995	0.690476	4760	27.3563	28	21	33
1	2	49	191.89	384.491	163	1.86387	0.84389	14.4062	0.926136	0.679167	4539	27.8466	29	22	33
1	2	50	201.221	456.572	145	1.33621	0.663261	13.5875	0.941558	0.690476	4681	32.2828	33	24	40
1	2	51	201.162	356.396	111	1.70636	0.810281	11.8882	0.880952	0.69375	4314	38.8649	41	31	45
1	2	52	204.031	41.5031	163	2.01967	0.868819	14.4062	0.910615	0.740909	4510	27.6687	30	23	33
1	2	53	206.779	234.517	145	1.69903	0.808446	13.5875	0.90625	0.710784	4665	32.1724	33	25	39
1	2	54	209.482	328.447	114	1.21621	0.569165	12.0478	0.926829	0.730769	4550	39.9123	41	31	48
1	2	55	218.386	102.956	158	1.97132	0.861784	14.1835	0.934911	0.619608	4640	29.3671	31	23	35
1	2	56	218.981	432.981	157	2.05395	0.873476	14.1386	0.902299	0.635628	4489	28.5924	30	23	34
1	2	57	221.277	471.106	141	1.42444	0.712149	13.3988	0.933775	0.801136	4526	32.0993	33	25	39
1	2	58	221.709	401.149	134	1.06894	0.353312	13.0619	0.911565	0.736264	4524	33.7612	35	26	42
1	2	59	222.761	129.858	113	1.23854	0.590005	11.9948	0.904	0.733766	5226	46.2478	48	36	55

1	2	60	223.098	346.61	123	1.19435	0.546784	12.5143	0.924812	0.732143	4533	36.8537	38	29	44
1	2	61	231.901	273.099	171	1.87159	0.845292	14.7555	0.924324	0.7125	5687	33.2573	35	26	40
1	2	62	230.337	380.573	178	1.64435	0.793828	15.0545	0.927083	0.698039	4786	26.8876	28	21	34
1	2	63	233.936	63.4295	298	1.96264	0.860461	19.4788	0.849003	0.620833	9681	32.4866	34	26	39
1	2	64	243.615	495.715	480	1.27632	0.621387	24.7215	0.933852	0.689655	23344	48.6333	52	40	58
1	2	65	239.465	27.8994	159	1.59375	0.778656	14.2283	0.908571	0.668067	6050	38.0503	39	29	47
1	2	66	238.785	118.85	107	1.3017	0.640175	11.672	0.90678	0.748252	5042	47.1215	48	39	56
1	2	67	248.411	107.352	219	1.76031	0.822971	16.6985	0.8327	0.608333	10494	47.9178	50	38	59
1	2	68	248.387	240.387	163	1.1782	0.528789	14.4062	0.936782	0.77619	4802	29.4601	31	22	35
1	2	69	251.401	459.551	147	1.36285	0.679415	13.6809	0.924528	0.765625	5259	35.7755	37	28	44
1	2	70	252.144	48.2734	139	1.28227	0.625943	13.3034	0.914474	0.772222	6892	49.5827	51	39	60
1	2	71	265.238	469.394	160	1.46715	0.731733	14.273	0.924855	0.784314	5318	33.2375	35	28	38
1	2	72	270.909	422.169	516	3.69314	0.962643	25.6318	0.786585	0.565789	24246	46.9884	48	34	60
1	2	73	273.05	102.567	201	2.48028	0.915121	15.9975	0.922018	0.644231	5194	25.8408	27	19	32
1	2	74	275.753	332.912	170	1.84216	0.839835	14.7123	0.918919	0.708333	4889	28.7588	30	21	37
1	2	75	282.79	24.8535	157	1.45739	0.727454	14.1386	0.94012	0.769608	8907	56.7325	59	46	68
1	2	76	304.73	201.073	178	1.19701	0.549623	15.0545	0.92228	0.747899	9829	55.2191	56	41	68
1	2	77	305.481	484.962	185	2.0845	0.877415	15.3476	0.91133	0.629252	4596	24.8432	26	19	30
1	2	78	307.247	40.9177	158	1.24996	0.599963	14.1835	0.934911	0.759615	5031	31.8418	34	26	37
1	2	79	308.276	329.299	127	1.83279	0.838036	12.7162	0.900709	0.661458	4575	36.0236	37	27	44
1	2	80	310.67	141.898	176	1.86898	0.84482	14.9696	0.931217	0.651852	4921	27.9602	29	21	34
1	2	81	315.681	247.266	229	1.52513	0.755038	17.0755	0.923387	0.726984	10311	45.0262	47	34	55
1	2	82	314.676	302.312	170	1.42819	0.713958	14.7123	0.923913	0.714286	4865	28.6176	29	23	35
1	2	83	320.461	216.509	228	1.37765	0.687826	17.0382	0.938272	0.76	10187	44.6798	46	37	53
1	2	84	320.624	423.867	226	3.36105	0.954714	16.9633	0.896825	0.434615	4603	20.3673	21	15	25
1	2	85	319.458	376.38	216	2.73428	0.930722	16.5837	0.892562	0.54	4741	21.9491	22	17	27
1	2	86	323.423	62.6264	182	1.43137	0.715481	15.2227	0.923858	0.722222	9774	53.7033	57	43	63
1	2	87	340.016	384.683	246	2.34015	0.904099	17.6979	0.81457	0.630769	9905	40.2642	43	32	49
1	2	88	344.4	270.337	285	1.43643	0.717877	19.0492	0.931373	0.714286	10324	36.2246	37	29	44
1	2	89	340.84	65.4787	94	1.19007	0.542146	10.94	0.903846	0.712121	4464	47.4894	51	37	57
1	2	90	341.06	478.91	134	2.01084	0.867577	13.0619	0.937063	0.783626	4299	32.0821	33	25	39
1	2	91	345.369	334.047	149	1.10502	0.425497	13.7736	0.925466	0.760204	4761	31.953	33	24	39
1	2	92	357.892	371.092	249	1.84813	0.840967	17.8055	0.932584	0.691667	6568	26.3775	27	21	33
1	2	93	354.205	391.672	122	1.46764	0.731944	12.4634	0.917293	0.67033	9313	76.3361	82	63	89
1	2	94	353.903	77.2419	124	1.57831	0.773669	12.5651	0.892086	0.688889	4741	38.2339	40	30	46
1	2	95	355.409	136.509	110	1.44194	0.720445	11.8345	0.916667	0.785714	4501	40.9182	42	32	49
1	2	96	361.412	208.768	194	1.20688	0.559863	15.7165	0.932692	0.760784	7985	41.1598	43	32	50
1	2	97	363.681	417.549	113	2.73659	0.930843	11.9948	0.849624	0.523148	2950	26.1062	26	16	36
1	2	98	370.626	159.489	131	1.56713	0.769945	12.9149	0.949275	0.81875	4759	36.3282	37	29	43
1	2	99	373.978	497.422	225	1.84477	0.840332	16.9257	0.918367	0.669643	9414	41.84	43	33	52
1	2	100	375.192	63.568	125	1.35274	0.673444	12.6157	0.932836	0.739645	4708	37.664	39	30	46
1	2	101	372	428.5	6	1.5	0.745356	2.76395	1	1	54	9	8	8	11
1	2	102	375.31	461.469	113	2.32052	0.902381	11.9948	0.862595	0.627778	2648	23.4336	24	17	30
1	2	103	372	441	1	1	0	1.12838	1	1	9	9	9	9	9
1	2	104	380.145	395.421	145	1.61066	0.783919	13.5875	0.917722	0.697115	4480	30.8966	32	24	38
1	2	105	384.421	107.916	202	1.72134	0.813944	16.0373	0.874459	0.590643	8500	42.0792	42	29	54
1	2	106	385.749	314.015	195	1.58739	0.776623	15.757	0.924171	0.684211	9749	49.9949	52	38	63
1	2	107	394.915	294.683	82	1.56076	0.767781	10.2179	0.87234	0.630769	7836	95.561	100	77	114
1	2	108	407.296	388.112	179	1.93382	0.855918	15.0967	0.92268	0.639286	4942	27.6089	28	20	36
1	2	109	405.333	167.802	162	1.96376	0.860631	14.3619	0.9	0.609023	4778	29.4938	31	22	36
1	2	110	405.662	54.9615	130	1.23602	0.587746	12.8655	0.915493	0.714286	4523	34.7923	36	27	42
1	2	111	409	479.357	129	1.86558	0.844201	12.8159	0.895833	0.614286	4429	34.3333	37	26	42
1	2	112	418.228	100.644	180	1.28967	0.631482	15.1388	0.891089	0.705882	7824	43.4667	47	33	53
1	2	113	426.611	225.589	270	1.81845	0.835218	18.5412	0.891089	0.613636	9758	36.1407	38	28	44
1	2	114	423.62	401.364	129	1.41093	0.705455	12.8159	0.902098	0.716667	4596	35.6279	37	27	43
1	2	115	425.799	183.281	139	1.85684	0.842594	13.3034	0.908497	0.620536	4569	32.8705	35	25	40
1	2	116	429.85	439.218	206	1.51878	0.752647	16.1953	0.936364	0.774436	7146	34.6893	35	26	43
1	2	117	425.908	491.557	131	1.44763	0.723062	12.9149	0.916084	0.744318	6530	49.8473	53	37	60
1	2	118	434.543	58.8768	138	1.25228	0.601938	13.2555	0.926174	0.704082	4540	32.8986	35	26	39
1	2	119	439.22	364.115	218	2.32616	0.90288	16.6603	0.875502	0.605556	9123	41.8486	43	33	52
1	2	120	433.784	385.392	51	1.25129	0.601101	8.05824	0.944444	0.796875	3773	73.9804	72	60	89
1	2	121	436.309	477.414	152	1.08643	0.390878	13.9116	0.91018	0.72381	4444	29.2368	30	23	35
1	2	122	446.156	154.905	147	1.93636	0.856328	13.6809	0.93038	0.773684	4785	32.551	34	25	39
1	2	123	448.056	77.784	162	1.62655	0.788684	14.3619	0.9	0.710526	4549	28.0802	30	22	34
1	2	124	446.81	389.738	42	1.13949	0.479424	7.31273	0.893617	0.75	3482	82.9048	87	67	104
1	2	125	452.475	39.766	141	1.56502	0.769232	13.3988	0.933775	0.734375	8316	58.9787	61	47	71
1	2	126	457.992	123.558	129	1.35097	0.672379	12.8159	0.921429	0.732955	4753	36.845	38	27	46
1	2	127	457.669	492.056	124	1.37051	0.683818	12.5651	0.918519	0.751515	4109	33.1371	34	26	41
1	2	128	462.252	30.4967	151	1.62568	0.788427	13.8658	0.937888	0.725962	7643	50.6159	53	40	60
1	2	129	466.371	220.547	232	1.63718	0.791781	17.187	0.924303	0.682353	9151	39.444	41	31	48
1	2	130	478.772	77.88	250	3.50476	0.958431	17.8412	0.859107	0.434783	9444	37.776	38	29	47
1	2	131	472.497	344.745	145	1.74711	0.819994	13.5875	0.889571	0.69378	4916	33.9034	35	27	41
1	2	132	474.284	440.578	109	1.72316	0.814383	11.7806	0.923729	0.707792	4014	36.8257	39	29	43
1	2	133	475.31	456.124	113	1.32543	0.656329	11.9948	0.918699	0.733766	3961	35.0531	37	28	42
1	2	134	474.222	407.025	81	1.22039	0.573208	10.1554	0.9	0.736364	2413	29.7901	32	24	36
1	2	135	491.61	192.063	205	2.29749	0.900306	16.1559	0.931818	0.776515	5209	25.4098	26	19	32

1	2	136	485.88	366.669	299	2.80072	0.934085	19.5115	0.89521	0.68894	14065	47.0401	50	38	57
1	2	137	488.732	106.247	190	1.75179	0.821058	15.5536	0.855856	0.666667	8786	46.2421	50	35	57
1	2	138	492.338	317.287	195	1.3628	0.679385	15.757	0.933014	0.77381	5408	27.7333	29	23	34
1	3	1	10.098	359.078	102	1.21521	0.56818	11.3961	0.918919	0.713287	5508	54	58	39	68
1	3	2	14.7415	119.565	147	1.8992	0.850152	13.6809	0.88024	0.576471	5099	34.6871	37	25	44
1	3	3	16.517	274.364	176	1.49674	0.744054	14.9696	0.926316	0.647059	9866	56.0568	60	45	68
1	3	4	13	374.451	82	1.20928	0.562296	10.2179	0.88172	0.683333	4420	53.9024	56	46	64
1	3	5	23.1517	323.427	211	1.49712	0.744206	16.3907	0.905579	0.703333	9538	45.2038	47	35	55
1	3	6	22.7297	353.041	74	1.16551	0.513657	9.70668	0.880952	0.747475	4079	55.1216	56	44	66
1	3	7	23.7391	366.87	69	1.44756	0.723029	9.37302	0.873418	0.69697	3983	57.7246	59	48	70
1	3	8	34.5623	50.4478	297	2.56212	0.920687	19.4461	0.838983	0.53902	11784	39.6768	41	31	48
1	3	9	33.9742	109.832	155	1.63061	0.789875	14.0482	0.933735	0.691964	4887	31.529	33	24	39
1	3	10	44.7725	455.738	233	1.9878	0.864246	17.224	0.869403	0.647222	9369	40.2103	42	31	50
1	3	11	51.9162	275.366	191	1.67447	0.80209	15.5945	0.896714	0.636667	9954	52.1152	54	42	62
1	3	12	62.4292	263.297	219	1.22958	0.581865	16.6985	0.862205	0.608333	9759	44.5616	46	36	54
1	3	13	65.7559	171.244	213	2.19727	0.890435	16.4682	0.946667	0.806818	7486	35.1455	36	27	43
1	3	14	63.4132	488.702	121	1.69052	0.806279	12.4122	0.923664	0.75625	4267	35.2645	37	28	43
1	3	15	73.3548	80.7742	155	1.30361	0.64153	14.0482	0.922619	0.745192	9280	59.871	62	50	71
1	3	16	79	329.552	183	1.97089	0.861719	15.2644	0.915	0.72619	4967	27.1421	28	21	33
1	3	17	80.0286	183.648	210	1.64688	0.794543	16.3518	0.929204	0.714286	7257	34.5571	37	27	41
1	3	18	79.6596	291.823	141	1.25467	0.603949	13.3988	0.933775	0.783333	4830	34.2553	36	27	40
1	3	19	80.1048	310.169	124	1.39545	0.697472	12.5651	0.925373	0.751515	4607	37.1532	38	30	44
1	3	20	86.0366	103.451	164	1.55708	0.766515	14.4503	0.916201	0.689076	5296	32.2927	34	25	39
1	3	21	90.3161	139.787	174	1.67033	0.800986	14.8843	0.920635	0.654135	4690	26.954	29	21	32
1	3	22	85.1818	504.591	22	1.58172	0.774787	5.29257	0.916667	0.733333	1517	68.9545	68	64	76
1	3	23	88.5814	72.4186	43	1.89078	0.848695	7.39928	0.914894	0.671875	6443	149.837	155	105	186
1	3	24	95.9043	437.878	188	1.46558	0.731051	15.4716	0.930693	0.706767	4330	23.0319	23	18	28
1	3	25	103.775	259.664	271	2.25576	0.896369	18.5755	0.73842	0.531373	10362	38.2362	40	30	47
1	3	26	101.716	351.385	109	1.36499	0.680653	11.7806	0.923729	0.778571	4566	41.8899	44	33	52
1	3	27	100.971	381.4	105	1.68452	0.804731	11.5624	0.913043	0.673077	4538	43.219	45	34	53
1	3	28	102.731	26.3077	182	1.46207	0.729519	15.2227	0.938144	0.722222	5335	29.3132	31	24	35
1	3	29	108.742	241.381	252	1.52887	0.756426	17.9125	0.818182	0.666667	10076	39.9841	43	31	49
1	3	30	107.862	297.946	130	1.2305	0.58271	12.8655	0.928571	0.722222	4831	37.1615	37	29	46
1	3	31	117.68	139.313	128	1.2113	0.564315	12.7662	0.941176	0.761905	4503	35.1797	38	28	42
1	3	32	117.676	420.503	145	1.53776	0.759681	13.5875	0.91195	0.710784	3963	27.331	28	21	34
1	3	33	119.99	374.808	104	1.58258	0.775068	11.5073	0.912281	0.675325	4622	44.4423	45	34	55
1	3	34	124.631	466.313	160	2.13828	0.883905	14.273	0.855615	0.666667	3953	24.7063	25	19	31
1	3	35	125.541	492.842	133	1.14799	0.491128	13.0131	0.93007	0.730769	3821	28.7293	30	23	34
1	3	36	129.158	286.64	114	1.81038	0.833599	12.0478	0.919355	0.791667	4570	40.0877	42	31	49
1	3	37	135.662	301.387	80	1.7702	0.825154	10.0925	0.898876	0.714286	4315	53.9375	55	42	67
1	3	38	144.778	93.2454	216	1.26728	0.614272	16.5837	0.935065	0.75	8028	37.1667	39	30	44
1	3	39	144.088	361.596	114	1.78966	0.829327	12.0478	0.912	0.626374	4590	40.2632	42	32	49
1	3	40	147.37	232.151	119	1.2221	0.574839	12.3092	0.922481	0.772727	8226	69.1261	72	52	83
1	3	41	150.157	435.098	102	1.36069	0.678155	11.3961	0.910714	0.713287	3854	37.7843	40	31	45
1	3	42	154.435	412.167	108	1.47096	0.733373	11.7265	0.915254	0.701299	4156	38.4815	40	30	46
1	3	43	158.445	295.772	254	2.29656	0.90022	17.9834	0.84106	0.529167	9778	38.4961	40	31	48
1	3	44	159.99	30.2537	201	1.64383	0.793681	15.9975	0.934884	0.705263	6992	34.7861	36	27	42
1	3	45	159.799	272.021	144	1.23912	0.590519	13.5406	0.923077	0.738462	9195	63.8542	69	52	76
1	3	46	166.637	390.408	267	1.65549	0.796946	18.4379	0.946809	0.794643	10521	39.4045	41	29	49
1	3	47	170.118	433.126	119	1.42923	0.714457	12.3092	0.915385	0.708333	4156	34.9244	36	26	43
1	3	48	174.639	471.702	191	1.36363	0.679866	15.5945	0.945545	0.757937	8388	43.9162	45	36	52
1	3	49	175.864	132.604	154	1.35535	0.675001	14.0028	0.927711	0.733333	6793	44.1104	46	34	54
1	3	50	182.242	74.0719	153	1.41914	0.709554	13.9573	0.921687	0.75	4953	32.3725	34	26	38
1	3	51	188.486	428.514	144	2.14718	0.884928	13.5406	0.89441	0.571429	4506	31.2917	33	23	39
1	3	52	196.816	173.406	293	1.59008	0.777488	19.3147	0.904321	0.636957	21249	72.5222	74	57	89
1	3	53	194.99	340.259	286	1.78224	0.827754	19.0826	0.925566	0.733333	10276	35.9301	37	29	43
1	3	54	202.502	293.631	293	2.40846	0.909729	19.3147	0.84438	0.631466	10024	34.2116	36	26	42
1	3	55	206.054	40.8423	222	1.32324	0.654892	16.8125	0.936709	0.778947	9681	43.6081	46	34	53
1	3	56	218.937	319.989	269	1.78272	0.827856	18.5068	0.896667	0.68798	10198	37.9108	40	30	45
1	3	57	217.344	409.796	250	1.92424	0.854357	17.8412	0.816993	0.548246	9609	38.436	39	29	48
1	3	58	215.452	102.911	157	1.45643	0.727025	14.1386	0.928994	0.769608	6078	38.7134	40	31	46
1	3	59	221.224	468.737	304	1.81246	0.834019	19.674	0.87106	0.603175	20052	65.9605	70	51	81
1	3	60	224.342	36.0872	149	1.27651	0.621533	13.7736	0.93125	0.776042	4599	30.8658	33	25	36
1	3	61	228.918	451.459	159	1.38781	0.693392	14.2283	0.924419	0.719457	4908	30.8679	32	25	37
1	3	62	236.586	365.865	237	1.34179	0.666762	17.3712	0.846429	0.658333	5845	24.6624	25	18	31
1	3	63	235.433	13.5773	97	1.53429	0.758418	11.1132	0.941748	0.769841	4282	44.1443	47	32	54
1	3	64	238.177	54.8398	181	1.30302	0.641115	15.1808	0.928205	0.760504	4749	26.2376	28	21	32
1	3	65	242.074	491.788	189	1.66383	0.799233	15.5126	0.935644	0.726923	4786	25.3228	26	21	30
1	3	66	239.109	254.516	128	1.27034	0.61671	12.7662	0.914286	0.761905	5025	39.2578	41	31	45
1	3	67	245.439	301.049	285	1.7139	0.81214	19.0492	0.940594	0.652174	8867	31.1123	32	25	37
1	3	68	244.548	442.484	155	1.8373	0.838906	14.0482	0.922619	0.717593	4694	30.2839	32	25	36
1	3	69	252.391	36.7091	110	1.05333	0.314159	11.8345	0.92437	0.763889	4359	39.6273	41	33	48
1	3	70	260.993	69.3094	139	1.93453	0.856033	13.3034	0.902597	0.579167	4647	33.4317	34	26	41
1	3	71	260.8	238.867	75	1.38481	0.691768	9.77205	0.882353	0.694444	8191	109.213	109	86	132
1	3	72	260.881	465.983	59	1.68172	0.804	8.66724	0.867647	0.59596	7107	120.458	121	74	167
1	3	73	265.891	16.1091	110	1.34989	0.671725	11.8345	0.92437	0.769231	4628	42.0727	44	33	51

1	3	74	270.921	433.627	177	1.27986	0.624112	15.0121	0.917098	0.743697	9749	55.0791	55	42	69
1	3	75	273.484	87.2443	221	1.7298	0.815964	16.7746	0.884	0.613889	9572	43.3122	45	33	53
1	3	76	273.822	345.875	208	2.53252	0.91874	16.2737	0.908297	0.619048	9810	47.1635	49	36	57
1	3	77	287.91	395.184	488	2.04761	0.872635	24.9267	0.741641	0.530435	15133	31.0102	32	24	38
1	3	78	282.431	190.639	144	1.86664	0.844395	13.5406	0.9	0.666667	7827	54.3542	56	42	68
1	3	79	288.361	256.084	249	2.68567	0.928094	17.8055	0.778125	0.523109	10486	42.1124	43	33	51
1	3	80	280.085	492.603	189	1.23762	0.589177	15.5126	0.921951	0.75	4743	25.0952	27	20	30
1	3	81	283.268	23.6071	112	1.49137	0.741889	11.9416	0.888889	0.622222	4842	43.2321	47	26	59
1	3	82	286.84	279.133	293	1.2224	0.575125	19.3147	0.951299	0.820728	13463	45.9488	47	36	56
1	3	83	286.947	64.0877	114	1.53691	0.759372	12.0478	0.890625	0.690909	4589	40.2544	40	31	49
1	3	84	294.161	204.621	124	1.51011	0.749323	12.5651	0.939394	0.826667	6013	48.4919	51	39	57
1	3	85	294.434	349.69	129	1.33034	0.659521	12.8159	0.902098	0.716667	6258	48.5116	51	39	58
1	3	86	299	473.056	234	1.32743	0.657635	17.2609	0.83871	0.724458	8552	36.547	38	28	44
1	3	87	299.08	329.593	113	1.60776	0.783031	11.9948	0.896825	0.620879	5052	44.708	47	36	54
1	3	88	305.782	148.492	238	1.37652	0.687198	17.4078	0.929688	0.695906	10710	45	47	35	54
1	3	89	308.422	376.07	128	1.92602	0.85465	12.7662	0.927536	0.790123	4686	36.6094	38	28	45
1	3	90	310.653	41.0155	323	1.64555	0.794166	20.2795	0.828205	0.621154	9695	30.0155	29	21	43
1	3	91	317.211	458.408	473	1.49285	0.742486	24.5406	0.852252	0.615885	16175	34.1966	35	25	42
1	3	92	310.3	258.74	100	1.66277	0.798943	11.2838	0.900901	0.714286	4875	48.75	51	38	58
1	3	93	316.394	172.431	109	1.70657	0.810332	11.7806	0.939655	0.807407	4791	43.9541	46	34	54
1	3	94	319.03	158.242	99	1.44078	0.719907	11.2272	0.908257	0.692308	4732	47.798	49	39	58
1	3	95	320.597	216.664	134	1.40176	0.700768	13.0619	0.930556	0.812121	4915	36.6791	37	28	46
1	3	96	330.547	267.986	139	1.17331	0.523073	13.3034	0.926667	0.763736	5010	36.0432	36	28	46
1	3	97	337.579	327.823	271	2.09271	0.878442	18.5755	0.808955	0.6775	10198	37.631	40	29	46
1	3	98	333.177	395.24	192	1.71739	0.81299	15.6353	0.868778	0.627451	10244	53.3542	54	41	66
1	3	99	331.564	104.017	172	1.60903	0.783419	14.7986	0.924731	0.754386	9942	57.8023	60	48	69
1	3	100	338.308	360.632	133	1.15582	0.501454	13.0131	0.923611	0.791667	5241	39.406	40	31	47
1	3	101	342.452	380.048	124	1.40329	0.701558	12.5651	0.918519	0.681319	5215	42.0565	45	33	51
1	3	102	351.184	235.709	179	1.78723	0.828814	15.0967	0.899497	0.619377	5078	28.3687	29	22	35
1	3	103	349.87	267.807	161	1.21395	0.566948	14.3175	0.947059	0.825641	5106	31.7143	32	24	38
1	3	104	355.573	192.699	206	1.75463	0.8217	16.1953	0.919643	0.64375	7796	37.8447	38	29	47
1	3	105	362.143	124.473	357	1.5789	0.773864	21.3201	0.798658	0.686538	19382	54.2913	57	40	67
1	3	106	365.192	19.6384	177	1.28705	0.629539	15.0121	0.931579	0.743697	4816	27.209	29	21	33
1	3	107	364.781	79.4298	114	1.06965	0.354947	12.0478	0.912	0.730769	4537	39.7982	40	29	50
1	3	108	364.542	350.4	120	1.4471	0.722819	12.3608	0.944882	0.8	4689	39.075	40	32	46
1	3	109	368.913	285.978	46	1.36368	0.679896	7.65304	0.884615	0.638889	6786	147.522	151	117	181
1	3	110	380.866	338.11	127	1.10286	0.421706	12.7162	0.913669	0.751479	4777	37.6142	40	30	46
1	3	111	381.023	50.5496	131	1.54783	0.76328	12.9149	0.916084	0.744318	4369	33.3511	34	27	40
1	3	112	384.055	301.782	165	1.49253	0.74236	14.4943	0.953757	0.808824	9802	59.4061	62	48	70
1	3	113	386.369	106.795	195	2.07424	0.876114	15.757	0.933014	0.770751	5143	26.3744	28	19	33
1	3	114	398.813	384.067	134	1.35801	0.676576	13.0619	0.937063	0.812121	4920	36.7164	39	30	43
1	3	115	402.104	171.906	202	1.96693	0.861118	16.0373	0.918182	0.655844	5475	27.104	28	22	33
1	3	116	402.82	214.787	239	1.7078	0.810637	17.4443	0.895131	0.663889	13837	57.8954	58	43	74
1	3	117	407.701	469.368	117	1.49392	0.742919	12.2053	0.936	0.75974	4361	37.2735	39	29	46
1	3	118	412.597	72.0269	186	2.25991	0.896771	15.389	0.920792	0.673913	4700	25.2688	27	19	31
1	3	119	420.657	404.54	137	1.87173	0.845318	13.2073	0.913333	0.652381	6163	44.9854	48	36	54
1	3	120	421.21	439.79	100	1.74133	0.818664	11.2838	0.884956	0.666667	4125	41.25	42	32	51
1	3	121	421.597	210.642	67	1.77433	0.826053	9.23618	0.917808	0.697917	4008	59.8209	60	47	73
1	3	122	428.803	126.659	132	1.37134	0.684287	12.9641	0.923077	0.781065	4590	34.7727	35	27	43
1	3	123	428.429	468.696	112	1.35339	0.673829	11.9416	0.92562	0.8	4511	40.2768	42	33	48
1	3	124	440.679	30.7668	193	1.83016	0.837524	15.6759	0.919048	0.70696	4646	24.0725	25	19	29
1	3	125	441.736	399.443	246	1.39449	0.696963	17.6979	0.935361	0.719298	10094	41.0325	42	32	50
1	3	126	439.733	202.893	75	1.92194	0.85398	9.77205	0.872093	0.568182	4292	57.2267	61	44	71
1	3	127	439.909	324.977	44	1.33845	0.664673	7.48482	0.956522	0.785714	6863	155.977	161	120	193
1	3	128	444.902	155.214	173	1.15723	0.503268	14.8415	0.920213	0.720833	4938	28.5434	30	22	35
1	3	129	445.937	448.147	95	1.25669	0.605633	10.9981	0.904762	0.730769	4531	47.6947	48	36	59
1	3	130	444.353	188.412	34	1.24166	0.592769	6.57952	0.85	0.708333	5614	165.118	176	108	219
1	3	131	447.062	79.8769	130	1.11577	0.443558	12.8655	0.928571	0.77381	4603	35.4077	38	28	42
1	3	132	449.534	47.0451	133	1.06714	0.349099	13.0131	0.904762	0.678571	4683	35.2105	36	27	42
1	3	133	450.026	354.36	114	1.28391	0.627186	12.0478	0.942149	0.74026	4701	41.2368	42	32	51
1	3	134	460.248	103.075	226	3.00305	0.942929	16.9633	0.784722	0.427221	8764	38.7788	31	24	42
1	3	135	451.634	476.634	71	1.27897	0.623433	9.50789	0.910256	0.788889	4160	58.5915	60	48	70
1	3	136	463.959	250.088	148	1.36367	0.679888	13.7273	0.936709	0.758974	5502	37.1757	38	29	44
1	3	137	466.043	56.1739	23	1.31472	0.649198	5.41152	0.851852	0.657143	2634	114.522	118	89	149
1	3	138	465.3	63.85	20	1.20283	0.555713	5.04627	0.833333	0.666667	2430	121.5	132	87	154
1	3	139	474.931	370.517	87	1.37483	0.686253	10.5248	0.878788	0.669231	5493	63.1379	66	51	77
1	3	140	478.665	164.937	158	1.39125	0.695242	14.1835	0.929412	0.77451	8738	55.3038	56	42	70
1	3	141	475.295	182.409	44	1.52203	0.753875	7.48482	0.916667	0.698413	6727	152.886	156	111	188
1	3	142	482.725	413.554	204	1.77691	0.826609	16.1165	0.898678	0.6	9379	45.9755	48	35	59
1	3	143	485.122	58.085	294	1.44407	0.721431	19.3477	0.869822	0.786096	17665	60.085	62	47	72
1	3	144	482.755	453.941	102	1.94739	0.858085	11.3961	0.902655	0.708333	5666	55.549	56	37	71
1	3	145	480.108	483.45	120	1.77476	0.826146	12.3608	0.909091	0.681818	4258	35.4833	36	27	44
1	3	146	483.899	116.449	158	1.2289	0.581235	14.1835	0.918605	0.705357	4655	29.462	30	22	36
1	3	147	496.56	345.393	298	1.53534	0.758803	19.4788	0.792553	0.627368	9905	33.2383	35	25	41
1	3	148	489.322	41.1724	87	1.17086	0.520149	10.5248	0.887755	0.725	3815	43.8506	46	35	52
1	3	149	495.5	469.406	128	1.50512	0.747379	12.7662	0.934307	0.8	4444	34.7188	35	25	43

1	3	150	491.686	286.086	35	1.18938	0.541385	6.67558	0.945946	0.833333	3545	101.286	105	89	117
1	3	151	497.438	76.3769	130	2.04206	0.871891	12.8655	0.902778	0.637255	4553	35.0231	36	26	43
1	3	152	499.836	144.508	128	1.24075	0.591964	12.7662	0.920863	0.711111	4856	37.9375	39	30	46
1	3	153	504.436	285.462	39	1.4304	0.715017	7.04673	0.906977	0.8125	3680	94.359	96	79	113
1	4	1	20	122.671	152	1.3561	0.675449	13.9116	0.921212	0.730769	4832	31.7895	33	25	39
1	4	2	22.2081	72.3198	197	1.33473	0.662327	15.8376	0.929245	0.72963	9490	48.1726	50	37	59
1	4	3	22.1391	148.043	115	1.35777	0.676433	12.1005	0.92	0.746753	4511	39.2261	40	30	48
1	4	4	23.2774	287.022	137	1.66849	0.800492	13.2073	0.931973	0.805882	6042	44.1022	47	35	53
1	4	5	26.6026	348.245	151	1.68495	0.804842	13.8658	0.909639	0.699074	7260	48.0795	50	38	57
1	4	6	28.0294	162.559	102	1.28299	0.626493	11.3961	0.93578	0.784615	4532	44.4314	45	36	53
1	4	7	36.734	487.684	282	2.28224	0.898894	18.9487	0.817391	0.592437	9658	34.2482	35	26	43
1	4	8	39.2951	188.77	183	2.36982	0.906608	15.2644	0.905941	0.571875	4775	26.0929	27	19	33
1	4	9	49.5199	217.316	377	2.90967	0.939086	21.9092	0.821351	0.419355	15415	40.8886	35	26	60
1	4	10	40.3109	306.084	119	1.46635	0.731385	12.3092	0.929688	0.793333	4745	39.8739	41	29	49
1	4	11	49.8224	124.27	259	2.13833	0.883911	18.1595	0.799383	0.535124	10090	38.9575	41	30	48
1	4	12	53.6559	76.3118	186	1.22662	0.579108	15.389	0.944162	0.781513	9469	50.9086	53	42	60
1	4	13	61.75	496.487	156	1.3807	0.689518	14.0935	0.928571	0.764706	6401	41.0321	42	29	54
1	4	14	61.8438	110.813	96	1.5645	0.769055	11.0558	0.897196	0.671329	4500	46.875	49	38	56
1	4	15	70.6453	190.465	172	2.30563	0.901047	14.7986	0.900524	0.532508	5838	33.9419	35	27	41
1	4	16	69.6914	97.7778	81	1.43608	0.717712	10.1554	0.9	0.75	4431	54.7037	58	43	65
1	4	17	87.8529	100.461	102	1.86101	0.843364	11.3961	0.894737	0.708333	4364	42.7843	46	33	52
1	4	18	89.9259	68.8148	108	1.14834	0.491595	11.7265	0.915254	0.755245	4387	40.6204	43	33	46
1	4	19	98.8842	183.474	190	2.31245	0.901662	15.5536	0.92233	0.688406	7736	40.7158	42	32	49
1	4	20	98.8446	473.239	251	1.39113	0.695175	17.8769	0.933086	0.747024	10787	42.9761	46	34	51
1	4	21	96.8018	353.613	111	1.68667	0.805287	11.8882	0.917355	0.74	4686	42.2162	44	33	51
1	4	22	96.6612	405.521	121	1.31338	0.648287	12.4122	0.916667	0.785714	4595	37.9752	41	29	46
1	4	23	98.7228	41.5248	101	1.22405	0.576693	11.3401	0.90991	0.765152	4325	42.8218	44	33	52
1	4	24	100.188	110.136	176	1.48194	0.738011	14.9696	0.926316	0.739496	5059	28.7443	29	22	36
1	4	25	101.765	300.07	115	1.86325	0.843776	12.1005	0.884615	0.589744	4560	39.6522	41	31	49
1	4	26	108.133	141.793	135	1.06071	0.333452	13.1106	0.918367	0.741758	4866	36.0444	36	28	45
1	4	27	118.875	443.208	48	2.28411	0.899069	7.81764	0.774194	0.623377	5782	120.458	127	74	168
1	4	28	124.705	39.2679	112	1.95296	0.85896	11.9416	0.88189	0.622222	4383	39.1339	41	31	47
1	4	29	123.518	339.373	110	1.56515	0.769275	11.8345	0.92437	0.705128	4488	40.8	43	33	49
1	4	30	123.016	410.445	128	1.20716	0.560153	12.7662	0.907801	0.761905	4694	36.6719	37	29	45
1	4	31	130.864	80.248	125	1.35859	0.676922	12.6157	0.925926	0.757576	4636	37.088	38	28	45
1	4	32	135.846	109.582	182	1.19873	0.551436	15.2227	0.928571	0.764706	5123	28.1484	29	22	34
1	4	33	140.518	124.695	164	1.68308	0.804354	14.4503	0.921348	0.759259	4956	30.2195	31	24	36
1	4	34	141.5	164.779	104	1.25753	0.606338	11.5073	0.912281	0.722222	4404	42.3462	44	35	50
1	4	35	151.336	265.602	128	1.35544	0.675056	12.7662	0.907801	0.711111	4698	36.7031	39	30	44
1	4	36	154.318	473.529	157	1.65981	0.798134	14.1386	0.928994	0.654167	4848	30.879	31	25	38
1	4	37	153.259	431.776	116	1.73133	0.816326	12.153	0.892308	0.644444	4545	39.181	38	29	49
1	4	38	157.479	292.536	140	1.53578	0.758963	13.3512	0.915033	0.729167	4828	34.4857	35	27	43
1	4	39	160.654	163.442	156	1.03336	0.252051	14.0935	0.923077	0.742857	9609	61.5962	64	49	73
1	4	40	163.455	141	121	1.71923	0.813434	12.4122	0.896296	0.664835	4553	37.6281	39	29	46
1	4	41	164.635	45.5079	63	1.72672	0.815232	8.95623	0.913043	0.63	7016	111.365	116	91	136
1	4	42	168.561	331.11	82	1.63975	0.792517	10.2179	0.87234	0.621212	4075	49.6951	52	40	60
1	4	43	167.286	389.735	98	1.61962	0.786627	11.1704	0.882883	0.7	4307	43.949	46	35	52
1	4	44	171.548	93.6129	341	2.5791	0.921772	20.8369	0.833741	0.645833	14949	43.8387	45	33	55
1	4	45	170.747	210.678	87	1.21387	0.566864	10.5248	0.915789	0.790909	4778	54.9195	56	43	65
1	4	46	172.538	433.169	130	1.4418	0.72038	12.8655	0.915493	0.714286	4816	37.0462	37	29	46
1	4	47	182.654	195.457	81	1.03532	0.258957	10.1554	0.94186	0.81	4816	59.4568	60	45	71
1	4	48	188.789	451.247	194	1.86937	0.844891	15.7165	0.941748	0.734848	5054	26.0515	27	20	32
1	4	49	197.623	222.729	579	1.57599	0.772905	27.1515	0.772	0.486555	24028	41.4991	42	31	53
1	4	50	207.162	275.591	154	1.34856	0.670916	14.0028	0.933333	0.802083	7416	48.1558	51	37	56
1	4	51	208.366	19.4718	142	1.39993	0.699817	13.4462	0.922078	0.739583	4462	31.4225	32	24	39
1	4	52	216.594	153.421	254	1.67351	0.801835	17.9834	0.897527	0.636591	12587	49.5551	51	37	62
1	4	53	216.26	292.683	123	1.23562	0.587384	12.5143	0.911111	0.732143	7499	60.9675	63	51	73
1	4	54	223.36	332.144	125	1.10482	0.425139	12.6157	0.93985	0.801282	4674	37.392	38	29	44
1	4	55	224.5	17	8	1.19523	0.547723	3.19154	0.8	0.666667	82	10.25	11	6	14
1	4	56	235.095	181.581	241	2.2866	0.899301	17.5172	0.836806	0.617949	7444	30.888	32	22	39
1	4	57	230.172	402.352	128	1.20362	0.556529	12.7662	0.907801	0.65641	5212	40.7188	41	31	50
1	4	58	236.048	79.3832	167	1.40843	0.704192	14.5819	0.922652	0.755656	4581	27.4311	29	22	33
1	4	59	238.949	345.641	117	1.271	0.617231	12.2053	0.928571	0.75974	4616	39.453	41	30	48
1	4	60	241.222	378.852	81	1.37505	0.686378	10.1554	0.89011	0.75	6038	74.5432	78	59	87
1	4	61	252.197	247.61	385	3.61941	0.961075	22.1404	0.819149	0.49359	11357	29.4987	31	23	36
1	4	62	259.684	354.2	95	1.16027	0.507128	10.9981	0.88785	0.719697	4295	45.2105	47	38	54
1	4	63	268.622	143.438	315	1.83188	0.837859	20.0267	0.791457	0.686275	9714	30.8381	33	24	37
1	4	64	272.363	234.879	256	1.57039	0.771041	18.0541	0.911032	0.711111	8749	34.1758	34	28	42
1	4	65	271.957	343.086	93	1.42886	0.71428	10.8817	0.894231	0.704545	4324	46.4946	47	36	57
1	4	66	275.955	27.2211	199	1.5295	0.756659	15.9177	0.925581	0.690972	4521	22.7186	24	18	27
1	4	67	273.804	327.134	97	1.98725	0.864166	11.1132	0.873874	0.573964	4365	45	46	36	55
1	4	68	278.578	102.532	109	1.46495	0.730775	11.7806	0.886179	0.698718	5405	49.5872	50	37	63
1	4	69	279.534	305.602	103	1.37098	0.684081	11.4518	0.887931	0.72028	4411	42.8252	44	32	52
1	4	70	289.613	488.525	261	2.99776	0.942721	18.2295	0.852941	0.466071	9297	35.6207	36	27	46
1	4	71	283.109	451.764	55	1.69925	0.8085	8.36828	0.873016	0.611111	6359	115.618	120	91	142
1	4	72	290.576	78.3273	165	1.96088	0.860189	14.4943	0.932203	0.75	5053	30.6242	32	24	38

1	4	73	308.012	29.4471	170	1.2847	0.62778	14.7123	0.909091	0.674603	4598	27.0471	28	21	33
1	4	74	306.881	474.524	126	1.97041	0.861646	12.666	0.893617	0.6	4480	35.5556	38	28	43
1	4	75	310.799	253.669	299	1.49785	0.744498	19.5115	0.911585	0.679545	20353	68.0702	71	55	81
1	4	76	323.332	189.974	268	1.56218	0.768264	18.4724	0.867314	0.62037	9821	36.6455	39	27	46
1	4	77	320.089	159.349	169	1.58065	0.774437	14.6689	0.918478	0.722222	7397	43.7692	46	35	52
1	4	78	321.261	132.151	119	1.63076	0.789919	12.3092	0.929688	0.704142	4678	39.3109	41	29	48
1	4	79	331.813	442.724	123	1.51786	0.7523	12.5143	0.938931	0.82	4625	37.6016	39	30	44
1	4	80	341.061	46.986	358	1.87433	0.845786	21.3499	0.813636	0.587849	15309	42.7626	45	32	53
1	4	81	340.704	254.099	233	2.05836	0.874056	17.224	0.924603	0.716923	6864	29.4592	31	23	35
1	4	82	346.781	107.539	256	2.95122	0.940843	18.0541	0.864865	0.463768	7926	30.9609	33	24	38
1	4	83	346.119	140.637	160	1.20679	0.559777	14.273	0.914286	0.714286	5934	37.0875	39	29	45
1	4	84	350.881	77.457	151	1.13385	0.471336	13.8658	0.909639	0.719048	5405	35.7947	36	29	45
1	4	85	351.833	472.913	138	1.57445	0.772395	13.2555	0.92	0.737968	4717	34.1812	35	26	41
1	4	86	370.368	449.906	117	1.27551	0.620762	12.2053	0.914063	0.75974	4616	39.453	41	31	47
1	4	87	374.471	160.044	225	1.49907	0.744984	16.9257	0.929752	0.765306	9824	43.6622	45	32	54
1	4	88	376.337	504.93	86	1.25277	0.602348	10.4642	0.905263	0.781818	3841	44.6628	48	36	53
1	4	89	389.695	89.1684	190	1.2873	0.629721	15.5536	0.913462	0.745098	6740	35.4737	37	28	43
1	4	90	397.79	245.253	186	1.89957	0.850216	15.389	0.920792	0.664286	8465	45.5108	47	35	54
1	4	91	394.991	53.8739	111	1.61906	0.78646	11.8882	0.925	0.822222	4218	38	39	30	45
1	4	92	409.166	203.284	229	1.69096	0.806392	17.0755	0.946281	0.800699	9687	42.3013	44	34	51
1	4	93	404.844	33.6234	77	1.36656	0.681557	9.90149	0.950617	0.875	7522	97.6883	97	79	117
1	4	94	419.253	268.542	356	1.74772	0.820132	21.2902	0.872549	0.585526	12819	36.0084	37	28	44
1	4	95	408.808	16.7945	73	1.35563	0.675165	9.64088	0.890244	0.737374	7784	106.63	111	84	127
1	4	96	414.795	347.565	161	2.4258	0.911078	14.3175	0.894444	0.526144	5842	36.2857	37	27	46
1	4	97	414.418	47.1493	67	1.17547	0.525613	9.23618	0.905405	0.744444	4024	60.0597	62	47	71
1	4	98	413.019	491	107	2.86142	0.936945	11.672	0.829457	0.66875	3869	36.1589	34	25	49
1	4	99	420.868	128.549	144	1.4179	0.708939	13.5406	0.917197	0.75	4490	31.1806	33	24	37
1	4	100	423.104	104.057	106	1.43449	0.716964	11.6174	0.898305	0.627219	4077	38.4623	39	31	46
1	4	101	426.239	160.553	188	1.43937	0.719252	15.4716	0.930693	0.734375	8843	47.0372	49	36	58
1	4	102	425.926	63.8589	163	2.88936	0.938199	14.4062	0.835897	0.679167	8227	50.4724	48	35	65
1	4	103	438.319	109.233	116	1.445	0.72186	12.153	0.913386	0.70303	4171	35.9569	38	27	45
1	4	104	445.092	158.708	120	1.48149	0.73782	12.3608	0.916031	0.710059	4362	36.35	38	28	45
1	4	105	448.698	498.14	172	1.7764	0.826499	14.7986	0.924731	0.632353	4888	28.4186	30	21	35
1	4	106	455.915	28.6154	130	1.30643	0.643502	12.8655	0.928571	0.787879	6559	50.4538	53	40	61
1	4	107	462.451	83.2254	142	1.20737	0.560366	13.4462	0.928105	0.788889	6157	43.3592	46	35	52
1	4	108	470.954	328.27	152	2.62376	0.92452	13.9116	0.894118	0.5	4143	27.2566	30	20	33
1	4	109	465.05	462.9	20	1.08287	0.383662	5.04627	0.869565	0.8	58	2.9	3	1	4
1	4	110	473.657	118.641	245	1.49531	0.743482	17.6619	0.935115	0.720588	9593	39.1551	39	30	50
1	4	111	479.737	255.395	152	1.89314	0.849105	13.9116	0.921212	0.666667	5655	37.2039	39	29	45
1	4	112	489.175	433.893	309	1.50055	0.745576	19.8351	0.830645	0.588571	14140	45.7605	48	35	56
1	4	113	488.297	19.5034	145	1.7151	0.812432	13.5875	0.900621	0.647321	4612	31.8069	33	22	41
1	5	1	12.1124	81.2426	169	1.75774	0.822397	14.6689	0.89418	0.625926	5289	31.2959	33	24	38
1	5	2	21.6842	157.061	114	1.32558	0.656429	12.0478	0.890625	0.690909	4450	39.0351	41	30	47
1	5	3	26.5433	251.717	127	1.39677	0.698164	12.7162	0.913669	0.697802	4420	34.8031	35	27	42
1	5	4	33.697	139.273	132	1.66927	0.800701	12.9641	0.923077	0.6875	4555	34.5076	36	27	42
1	5	5	31.8739	216.532	111	1.64226	0.793234	11.8882	0.909836	0.770833	4359	39.2703	42	29	48
1	5	6	39.4234	413.721	222	1.28116	0.625105	16.8125	0.944681	0.687307	9624	43.3514	45	34	53
1	5	7	42.3592	301.33	103	1.85131	0.841564	11.4518	0.880342	0.64375	4366	42.3883	44	32	54
1	5	8	40.6712	471.441	222	1.66922	0.800686	16.8125	0.925	0.776224	9583	43.1667	44	33	53
1	5	9	46.598	35.2864	199	1.47235	0.733967	15.9177	0.934272	0.731618	9167	46.0653	48	37	54
1	5	10	52.8175	226.246	126	1.33284	0.661126	12.666	0.919708	0.763636	4550	36.1111	38	29	44
1	5	11	56.0102	81.1371	197	1.15958	0.506263	15.8376	0.938095	0.772549	8944	45.401	47	37	55
1	5	12	55.3209	345.187	134	1.09487	0.407181	13.0619	0.930556	0.736264	4700	35.0746	37	28	42
1	5	13	58.7305	465.979	141	1.46864	0.732373	13.3988	0.927632	0.671429	4519	32.0496	34	25	39
1	5	14	59.9231	102.546	130	1.06579	0.34589	12.8655	0.915493	0.769231	4593	35.3308	37	29	42
1	5	15	59.8505	253.991	107	1.52309	0.754275	11.672	0.884298	0.633136	4346	40.6168	42	33	50
1	5	16	77.2771	393.892	166	1.68073	0.80374	14.5381	0.948571	0.794258	8121	48.9217	52	40	57
1	5	17	75.5	213	106	1.52953	0.75667	11.6174	0.898305	0.688312	4366	41.1887	42	31	50
1	5	18	81.3667	139.839	180	1.37201	0.684667	15.1388	0.923077	0.714286	8487	47.15	49	37	57
1	5	19	78.669	245.197	142	1.7102	0.811229	13.4462	0.922078	0.759358	4639	32.669	33	25	40
1	5	20	80.7353	114.422	102	1.17952	0.530312	11.3961	0.910714	0.772727	4258	41.7451	44	34	49
1	5	21	85.9789	324.095	95	1.41567	0.707832	10.9981	0.904762	0.664336	4181	44.0105	45	36	54
1	5	22	89.9514	365.229	144	1.57597	0.772899	13.5406	0.917197	0.685714	4691	32.5764	34	26	39
1	5	23	89.4218	469.204	147	1.53767	0.759648	13.6809	0.907407	0.65625	4770	32.449	35	25	39
1	5	24	122.646	39.3708	178	1.24309	0.594028	15.0545	0.941799	0.741667	9293	52.2079	56	42	61
1	5	25	127.254	246.36	114	1.10719	0.429255	12.0478	0.926829	0.730769	4409	38.6754	40	31	47
1	5	26	143.249	122.979	233	2.33101	0.903306	17.224	0.906615	0.557416	9711	41.6781	43	34	50
1	5	27	185.285	178.486	144	1.42193	0.710922	13.5406	0.923077	0.75	5604	38.9167	41	32	45
1	5	28	190.814	79.4602	113	1.25241	0.60205	11.9948	0.918699	0.733766	4431	39.2124	40	31	47
1	5	29	193.435	196.613	168	1.65526	0.796882	14.6255	0.913043	0.65625	8079	48.0893	51	38	58
1	5	30	193.194	360.657	108	1.42453	0.71219	11.7265	0.915254	0.771429	4344	40.2222	41	31	50
1	5	31	205.619	335.608	97	1.53037	0.756983	11.1132	0.866071	0.621795	4188	43.1753	44	34	53
1	5	32	210.061	95.5338	148	1.67721	0.802814	13.7273	0.886228	0.669683	4698	31.7432	32	24	39
1	5	33	211.883	25.4	180	1.8842	0.847541	15.1388	0.913706	0.692308	8908	49.4889	53	40	58
1	5	34	233.203	73.9248	133	1.84276	0.83995	13.0131	0.93007	0.71123	4560	34.2857	35	26	41
1	5	35	243.053	255.215	685	1.7752	0.82624	29.5325	0.710581	0.465986	29016	42.3591	44	34	52

1	5	36	244.883	44.7186	334	1.70565	0.810104	20.6219	0.885942	0.703158	15694	46.988	49	38	55
1	5	37	246.434	115.89	145	1.57559	0.772771	13.5875	0.917722	0.697115	4689	32.3379	33	25	39
1	5	38	245.763	364.532	173	1.4535	0.725714	14.8415	0.905759	0.686508	9292	53.711	56	44	64
1	5	39	259.865	297.804	148	1.74551	0.819627	13.7273	0.907975	0.669683	6158	41.6081	44	33	50
1	5	40	265.892	35.5	186	1.69253	0.806796	15.389	0.925373	0.645833	7714	41.4731	44	34	50
1	5	41	267.611	474.84	288	1.69734	0.808018	19.1492	0.857143	0.626087	12451	43.2326	45	33	53
1	5	42	276.033	256.171	152	1.66024	0.798253	13.9116	0.91018	0.703704	6365	41.875	44	34	49
1	5	43	288.878	481.764	123	1.8018	0.831849	12.5143	0.91791	0.803922	4486	36.4715	38	29	43
1	5	44	295.075	442.753	146	1.6856	0.805009	13.6343	0.918239	0.737374	5724	39.2055	40	30	46
1	5	45	300.664	479.541	122	1.79398	0.830231	12.4634	0.917293	0.797386	4489	36.7951	39	30	43
1	5	46	318.606	113.228	254	1.95525	0.859316	17.9834	0.830065	0.574661	10021	39.4528	42	31	47
1	5	47	316.634	410.756	131	1.27616	0.621266	12.9149	0.89726	0.668367	7879	60.145	63	48	73
1	5	48	334.614	418.425	391	1.46851	0.732318	22.3123	0.807851	0.55698	18741	47.9309	47	36	62
1	5	49	339.399	87.0629	143	1.88512	0.847704	13.4935	0.910828	0.752632	4653	32.5385	34	27	38
1	5	50	346.493	100.553	219	2.21567	0.892357	16.6985	0.943966	0.796364	5193	23.7123	24	19	29
1	5	51	348.328	442.77	174	1.41208	0.706034	14.8843	0.935484	0.725	6367	36.592	37	30	44
1	5	52	356.336	138.177	232	1.8871	0.848052	17.187	0.939271	0.659091	5191	22.375	24	18	27
1	5	53	363.332	178.751	265	1.66527	0.799621	18.3687	0.886288	0.752841	11544	43.5623	45	36	52
1	5	54	368.601	52.3114	228	1.73712	0.817686	17.0382	0.919355	0.633333	9439	41.3991	43	33	50
1	5	55	372.972	19.7934	213	1.41274	0.706369	16.4682	0.938326	0.747368	9210	43.2394	44	32	54
1	5	56	374.753	117.607	150	1.29951	0.638622	13.8198	0.943396	0.78125	4877	32.5133	34	27	38
1	5	57	374.303	311.178	152	1.15034	0.494272	13.9116	0.921212	0.77551	4807	31.625	32	26	38
1	5	58	377.8	326.522	115	1.45456	0.726189	12.1005	0.912698	0.737179	4437	38.5826	40	30	46
1	5	59	378.921	363.124	266	1.84987	0.841294	18.4033	0.889632	0.738889	9883	37.1541	39	29	44
1	5	60	384.396	268.143	230	2.04748	0.872617	17.1127	0.916335	0.575	8281	36.0043	38	29	44
1	5	61	385.282	492.842	202	1.86295	0.84372	16.0373	0.935185	0.765152	8567	42.4109	45	34	51
1	5	62	410.504	429.727	139	1.74983	0.820613	13.3034	0.908497	0.620536	4291	30.8705	32	25	36
1	5	63	411.49	466.68	259	1.41752	0.708752	18.1595	0.945255	0.770833	9626	37.166	38	30	45
1	5	64	422.424	175.104	328	1.81488	0.834505	20.4358	0.81592	0.585714	10429	31.7957	35	25	38
1	5	65	443.127	154.822	353	1.61841	0.786264	21.2003	0.822844	0.613913	12182	34.5099	36	25	42
1	5	66	440.54	90.6832	202	1.37459	0.686118	16.0373	0.897778	0.701389	9021	44.6584	47	35	54
1	5	67	454.759	375.696	257	2.97619	0.941862	18.0893	0.859532	0.494231	9329	36.2996	38	27	45
1	5	68	452.566	444.485	136	1.59497	0.779044	13.159	0.92517	0.708333	4269	31.3897	33	25	38
1	5	69	464.612	335.218	294	1.32695	0.657325	19.3477	0.830508	0.608696	15405	52.398	55	40	63
1	5	70	468.948	264.647	326	1.6291	0.789433	20.3734	0.91573	0.686316	18203	55.8374	58	45	66
1	5	71	465.042	44.1354	96	1.9317	0.855575	11.0558	0.90566	0.623377	3616	37.6667	39	29	46
1	5	72	471.12	211.108	251	1.78261	0.827833	17.8769	0.922794	0.747024	9386	37.3944	39	30	45
1	5	73	466.162	66.9279	111	1.23308	0.585076	11.8882	0.909836	0.720779	4120	37.1171	39	29	45
1	5	74	472.917	140.042	168	1.49961	0.745199	14.6255	0.908108	0.658824	5693	33.8869	36	26	41
1	5	75	472.007	452	146	1.38385	0.691246	13.6343	0.929936	0.748718	4402	30.1507	32	25	36
1	5	76	480.38	161.804	158	1.088	0.393983	14.1835	0.923977	0.752381	6223	39.3861	43	31	46
1	5	77	483.022	324.5	228	1.49614	0.743814	17.0382	0.926829	0.705882	9761	42.8114	45	31	53
1	5	78	480.088	485.956	113	1.31461	0.649128	11.9948	0.918699	0.733766	4219	37.3363	39	30	44
1	5	79	484.238	427.325	126	1.78479	0.828297	12.666	0.926471	0.642857	4172	33.1111	35	27	40
1	5	80	488.556	365.677	124	1.60356	0.781734	12.5651	0.898551	0.632653	4430	35.7258	37	28	44
1	5	81	492.935	486.839	124	1.7483	0.820264	12.5651	0.925373	0.810458	4449	35.879	37	31	41
1	5	82	500.688	443.375	112	1.26825	0.615051	11.9416	0.896	0.717949	4260	38.0357	40	29	46
1	6	1	13.3247	32.0206	194	1.80457	0.832417	15.7165	0.889908	0.577381	5416	27.9175	30	20	35
1	6	2	10.9224	265.724	116	1.37589	0.686848	12.153	0.920635	0.753247	4490	38.7069	39	29	48
1	6	3	18.9744	454.487	117	1.20659	0.559577	12.2053	0.914063	0.692308	3922	33.5214	34	26	41
1	6	4	27.2042	342.218	142	1.54653	0.76282	13.4462	0.934211	0.759358	4693	33.0493	35	26	40
1	6	5	27.2273	359.023	220	1.04045	0.276128	16.7366	0.92437	0.718954	8697	39.5318	41	31	48
1	6	6	33.1343	143.623	499	3.10618	0.94676	25.2061	0.799679	0.567045	24853	49.8056	46	36	68
1	6	7	42.9868	116.072	152	1.23866	0.590105	13.9116	0.915663	0.730769	4796	31.5526	32	25	38
1	6	8	46.016	262.755	188	2.09621	0.878875	15.4716	0.890995	0.580247	8627	45.8883	46	36	58
1	6	9	55.7664	473.864	214	1.83381	0.838233	16.5068	0.918455	0.715719	9014	42.1215	44	33	51
1	6	10	54.8431	308.078	102	1.43966	0.719387	11.3961	0.886957	0.728571	4113	40.3235	42	31	49
1	6	11	63.0966	31.486	321	1.12537	0.45869	20.2166	0.865229	0.663223	16634	51.8193	53	38	65
1	6	12	59.014	79.3497	143	1.91324	0.852532	13.4935	0.928571	0.722222	4232	29.5944	31	24	36
1	6	13	60.8614	420.223	166	1.50226	0.746252	14.5381	0.937853	0.751131	4349	26.1988	27	20	32
1	6	14	65.6294	230.122	197	1.39788	0.698748	15.8376	0.938095	0.781746	8672	44.0203	45	34	55
1	6	15	66.0072	459.725	138	1.08544	0.388889	13.2555	0.926174	0.758242	4182	30.3043	32	23	36
1	6	16	74	100.5	118	1.41026	0.70512	12.2573	0.921875	0.786667	4250	36.0169	37	29	43
1	6	17	82.3861	153.073	316	2.04524	0.872317	20.0585	0.890141	0.681034	15035	47.5791	46	34	63
1	6	18	74.5	76.3	140	1.2011	0.553925	13.3512	0.927152	0.777778	4409	31.4929	33	26	37
1	6	19	75.0336	296.849	119	1.49162	0.741988	12.3092	0.922481	0.721212	4261	35.8067	37	28	44
1	6	20	96.0543	217.457	129	1.11079	0.435352	12.8159	0.934783	0.763314	4179	32.3953	34	25	39
1	6	21	96.313	242.878	115	1.36483	0.680563	12.1005	0.912698	0.746753	4088	35.5478	36	28	43
1	6	22	93.5352	279.803	71	1.32937	0.658893	9.50789	0.922078	0.806818	7242	102	100	82	128
1	6	23	96.1847	458.115	157	1.38708	0.692999	14.1386	0.928994	0.747619	3945	25.1274	26	19	32
1	6	24	99	83	125	1.30866	0.645047	12.6157	0.919118	0.757576	4957	39.656	42	32	48
1	6	25	105.341	129.121	91	2.17195	0.887703	10.7641	0.919192	0.758333	3734	41.033	41	28	52
1	6	26	109.549	347.043	162	1.8889	0.848367	14.3619	0.905028	0.736364	4389	27.0926	28	21	34
1	6	27	119.701	107.464	97	1.81146	0.833817	11.1132	0.898148	0.621795	3817	39.3505	42	30	49
1	6	28	124.658	71.4658	234	2.15452	0.885761	17.2609	0.795918	0.65	8432	36.0342	37	28	45
1	6	29	129.865	443.19	237	2.14178	0.88431	17.3712	0.929412	0.593985	9025	38.0802	39	30	46

1	6	30	132.584	470.016	250	1.71834	0.813219	17.8412	0.929368	0.657895	5098	20.392	21	16	25
1	6	31	128.67	178.226	115	1.36792	0.682339	12.1005	0.891473	0.69697	4161	36.1826	38	28	44
1	6	32	133.392	331.248	153	1.70893	0.810918	13.9573	0.910714	0.708333	4400	28.7582	29	22	35
1	6	33	129.828	361.081	99	1.51368	0.750701	11.2272	0.9	0.692308	4268	43.1111	45	34	51
1	6	34	135.862	376.505	196	1.68408	0.804616	15.7973	0.806584	0.640523	9241	47.148	49	37	59
1	6	35	136.281	415.62	171	1.60258	0.78143	14.7555	0.909574	0.678571	3972	23.2281	24	18	28
1	6	36	133.941	132	118	1.86552	0.844191	12.2573	0.914729	0.670455	4024	34.1017	36	26	42
1	6	37	143.395	40.8098	205	2.45832	0.913525	16.1559	0.923423	0.716783	4596	22.4195	24	17	28
1	6	38	136.271	497.308	107	2.61388	0.923925	11.672	0.89916	0.629412	4016	37.5327	38	28	47
1	6	39	141.448	248.271	181	1.38148	0.689946	15.1808	0.918782	0.709804	8458	46.7293	47	37	57
1	6	40	153.392	90.6022	181	1.20958	0.562598	15.1808	0.93299	0.760504	8163	45.0994	47	37	55
1	6	41	155.006	138.468	173	1.63706	0.791746	14.8415	0.910526	0.720833	7660	44.2775	45	35	53
1	6	42	154.19	371.076	105	1.57167	0.771469	11.5624	0.9375	0.777778	4529	43.1333	45	35	50
1	6	43	158.17	311.535	159	1.82167	0.835858	14.2283	0.913793	0.722727	4453	28.0063	29	21	35
1	6	44	163.866	62.5155	97	1.30584	0.643091	11.1132	0.92381	0.746154	4091	42.1753	45	35	50
1	6	45	163.836	193.575	73	1.19543	0.547937	9.64088	0.879518	0.663636	2333	31.9589	32	26	39
1	6	46	164.629	463.971	105	1.30539	0.642774	11.5624	0.905172	0.734266	4096	39.0095	40	30	48
1	6	47	168.383	77.1358	81	1.09668	0.410546	10.1554	0.89011	0.736364	3980	49.1358	50	40	60
1	6	48	171.28	161.194	93	1.48321	0.738536	10.8817	0.93	0.704545	3451	37.1075	39	30	43
1	6	49	171.794	405.46	126	1.15273	0.49743	12.666	0.933333	0.807692	3872	30.7302	32	24	37
1	6	50	171.641	492.672	128	1.87546	0.845987	12.7662	0.895105	0.627451	4145	32.3828	34	25	40
1	6	51	173.67	222.276	203	1.35599	0.675379	16.0769	0.931193	0.751852	8986	44.266	46	34	53
1	6	52	178.902	433.735	102	1.81242	0.83401	11.3961	0.87931	0.60355	4289	42.049	43	31	54
1	6	53	185.608	86.8987	237	2.75857	0.931981	17.3712	0.792642	0.50641	8974	37.865	41	29	47
1	6	54	194.827	300.864	162	1.81442	0.834412	14.3619	0.936416	0.77512	4457	27.5123	28	21	34
1	6	55	196.489	333.525	282	1.85588	0.842417	18.9487	0.88125	0.582645	9826	34.844	37	28	42
1	6	56	193.333	198.188	69	1.37758	0.68779	9.37302	0.907895	0.784091	2189	31.7246	33	24	39
1	6	57	197.394	480.986	142	1.38735	0.693144	13.4462	0.910256	0.682692	4317	30.4014	31	24	37
1	6	58	198.895	14.0349	172	1.53588	0.758998	14.7986	0.919786	0.671875	8451	49.1337	51	40	60
1	6	59	203.68	182.922	103	1.19441	0.546851	11.4518	0.927928	0.780303	4291	41.6602	44	34	50
1	6	60	203.9	144.811	90	1.15049	0.494473	10.7047	0.909091	0.743802	4030	44.7778	47	35	54
1	6	61	208.575	113.591	127	1.13094	0.467075	12.7162	0.894366	0.697802	4249	33.4567	34	25	43
1	6	62	211.252	442.087	127	1.54916	0.763752	12.7162	0.907143	0.721591	4218	33.2126	35	26	40
1	6	63	216.464	54.7969	192	1.19242	0.5447	15.6353	0.923077	0.705882	8652	45.0625	46	35	57
1	6	64	217.939	201.412	148	1.21036	0.563371	13.7273	0.930818	0.704762	6994	47.2568	50	39	57
1	6	65	216.628	175.738	164	1.70375	0.809629	14.4503	0.921348	0.784689	5629	34.3232	36	28	40
1	6	66	218.676	394.858	204	2.15034	0.885288	16.1165	0.910714	0.63354	4637	22.7304	24	18	27
1	6	67	220.865	350.827	104	1.29582	0.635975	11.5073	0.928571	0.722222	4228	40.6538	42	31	49
1	6	68	229.603	236.64	136	1.42958	0.714626	13.159	0.877419	0.653846	3947	29.0221	30	22	36
1	6	69	228.632	467.226	106	1.38212	0.690294	11.6174	0.890756	0.688312	4010	37.8302	39	31	46
1	6	70	240.147	249.049	143	2.56519	0.920885	13.4935	0.89375	0.525735	4059	28.3846	29	21	37
1	6	71	236.88	341.892	83	1.41995	0.709952	10.28	0.882979	0.709402	4079	49.1446	50	38	61
1	6	72	244.699	88.3706	143	1.38306	0.690813	13.4935	0.916667	0.744792	4294	30.028	31	23	37
1	6	73	251.232	18.672	125	1.2051	0.558056	12.6157	0.905797	0.744048	4150	33.2	34	27	40
1	6	74	253.463	309.288	80	1.63102	0.789994	10.0925	0.909091	0.740741	3944	49.3	51	39	61
1	6	75	257.025	44.1698	159	1.56254	0.76839	14.2283	0.929825	0.80303	4305	27.0755	28	21	33
1	6	76	259.014	278.879	140	1.7642	0.823835	13.3512	0.915033	0.625	4146	29.6143	31	22	37
1	6	77	257.368	332.333	87	1.40256	0.701183	10.5248	0.887755	0.725	4390	50.4598	51	38	63
1	6	78	258.629	167.266	124	1.03654	0.263166	12.5651	0.911765	0.733728	4215	33.9919	36	26	42
1	6	79	269.735	297.283	113	1.35843	0.676824	11.9948	0.904	0.733766	3856	34.1239	35	26	42
1	6	80	273.347	97.7288	118	1.47984	0.737133	12.2573	0.880597	0.648352	3983	33.7542	35	26	42
1	6	81	271.644	129.856	118	1.90244	0.850706	12.2573	0.893939	0.670455	3988	33.7966	35	26	41
1	6	82	281.493	495.375	296	2.40868	0.909746	19.4134	0.902439	0.560606	18228	61.5811	61	48	76
1	6	83	288.973	400.997	367	2.92475	0.939733	21.6166	0.882212	0.50551	14136	38.5177	40	31	47
1	6	84	280.48	201.696	125	1.10917	0.432621	12.6157	0.932836	0.801282	4211	33.688	35	26	41
1	6	85	289.615	433.563	96	1.49853	0.744771	11.0558	0.90566	0.738462	4561	47.5104	50	37	56
1	6	86	293.636	475.985	66	1.19599	0.548538	9.167	0.90411	0.733333	7232	109.576	112	84	134
1	6	87	299.794	390.016	126	2.50588	0.916924	12.666	0.9	0.736842	4331	34.373	35	26	43
1	6	88	304.173	264.688	301	1.1756	0.525765	19.5766	0.847887	0.651515	18051	59.9701	61	47	74
1	6	89	301.379	169.345	87	1.32239	0.654335	10.5248	0.90625	0.725	3930	45.1724	46	33	57
1	6	90	306.688	432.152	112	1.39275	0.696038	11.9416	0.903226	0.717949	4786	42.7321	45	33	51
1	6	91	305.333	335.758	33	1.52246	0.754039	6.48204	0.916667	0.673469	5488	166.303	170	138	199
1	6	92	310.047	193.859	128	1.81317	0.834161	12.7662	0.914286	0.609524	4232	33.0625	35	26	39
1	6	93	310.465	48.1628	129	1.19976	0.552515	12.8159	0.889655	0.661538	4033	31.2636	33	24	37
1	6	94	319.984	465.903	124	1.29066	0.63221	12.5651	0.925373	0.733728	4261	34.3629	35	26	42
1	6	95	325.932	374.111	235	1.86	0.843179	17.2977	0.925197	0.658263	8846	37.6426	39	29	47
1	6	96	324.701	433.828	87	1.30457	0.642199	10.5248	0.915789	0.725	4236	48.6897	51	41	56
1	6	97	325.081	446.453	86	1.70754	0.810574	10.4642	0.934783	0.826923	4283	49.8023	51	42	59
1	6	98	331.918	24.2634	243	2.42412	0.910948	17.5897	0.815436	0.54	8882	36.5514	37	27	45
1	6	99	331.821	91.5446	112	1.38632	0.692587	11.9416	0.918033	0.666667	4149	37.0446	39	30	43
1	6	100	332.461	151.078	128	1.36318	0.679607	12.7662	0.907801	0.711111	7759	60.6172	62	49	74
1	6	101	335.986	222.69	142	1.72276	0.814285	13.4462	0.934211	0.788889	4647	32.7254	34	26	39
1	6	102	350.636	153.236	110	1.39529	0.697386	11.8345	0.901639	0.714286	4340	39.4545	40	30	47
1	6	103	354.773	470.773	128	1.72519	0.814869	12.7662	0.927536	0.711111	4253	33.2266	34	25	41
1	6	104	356.548	434.774	217	1.67429	0.80204	16.6221	0.923404	0.758741	9279	42.7604	44	34	53
1	6	105	357.339	292.398	118	1.22631	0.578819	12.2573	0.914729	0.702381	4199	35.5847	37	28	44

1	6	106	359.018	312.36	114	1.78064	0.827412	12.0478	0.897638	0.626374	4181	36.6754	38	28	45
1	6	107	361.744	169.031	129	1.60135	0.781048	12.8159	0.908451	0.661538	7536	58.4186	60	46	71
1	6	108	370.42	126.786	112	1.12786	0.46247	11.9416	0.903226	0.717949	4218	37.6607	40	30	46
1	6	109	379.866	101.258	97	1.21577	0.568727	11.1132	0.898148	0.734848	4144	42.7216	44	34	51
1	6	110	382.727	404.684	187	1.74828	0.820259	15.4304	0.912195	0.611111	8630	46.1497	48	36	57
1	6	111	388.96	193.188	303	1.82054	0.835633	19.6416	0.907186	0.63125	11210	36.9967	39	29	45
1	6	112	387.155	337.23	174	1.75594	0.821995	14.8843	0.915789	0.725	8757	50.3276	52	39	61
1	6	113	384.868	261.441	136	1.68261	0.804233	13.159	0.894737	0.653846	4577	33.6544	35	27	41
1	6	114	401.428	302.432	414	1.51997	0.753099	22.9591	0.866109	0.613333	19684	47.5459	50	32	61
1	6	115	399.517	232.544	149	2.04919	0.872845	13.7736	0.925466	0.636752	5411	36.3154	38	29	44
1	6	116	414.693	273.039	384	1.50902	0.748901	22.1116	0.829374	0.601881	9995	26.0286	27	20	32
1	6	117	424.434	70.7862	159	1.6314	0.790105	14.2283	0.940828	0.80303	4592	28.8805	29	22	35
1	6	118	429	16	109	1.24326	0.594169	11.7806	0.931624	0.762238	3903	35.8073	37	30	42
1	6	119	434.508	178.295	132	1.38334	0.690966	12.9641	0.923077	0.733333	4152	31.4545	33	25	38
1	6	120	442.846	371.2	395	1.68433	0.80468	22.4261	0.951807	0.801217	10217	25.8658	26	20	31
1	6	121	435.648	108.209	91	1.42734	0.713551	10.7641	0.91	0.777778	3764	41.3626	43	33	51
1	6	122	439.969	245.641	131	1.74057	0.818488	12.9149	0.891156	0.727778	4284	32.7023	34	25	39
1	6	123	444.345	472.391	110	1.52612	0.755407	11.8345	0.92437	0.785714	4269	38.8091	40	29	47
1	6	124	447.904	87.8989	178	1.58428	0.775618	15.0545	0.92228	0.669173	4498	25.2697	27	20	30
1	6	125	450.265	488.54	113	1.37601	0.686912	11.9948	0.941667	0.807143	4363	38.6106	39	30	48
1	6	126	454.785	140.813	107	1.25762	0.606412	11.672	0.90678	0.748252	3888	36.3364	38	29	44
1	6	127	456.12	159.5	100	1.2749	0.620284	11.2838	0.925926	0.769231	3858	38.58	41	31	47
1	6	128	461.271	117.624	133	1.7004	0.808791	13.0131	0.875	0.59375	4162	31.2932	33	24	38
1	6	129	463.58	186.899	257	1.7078	0.810637	18.0893	0.911348	0.679894	9420	36.6537	38	28	46
1	6	130	472.762	297.525	101	1.12911	0.464354	11.3401	0.90991	0.765152	8080	80	79	63	98
1	6	131	477.607	138.476	145	1.23853	0.589992	13.5875	0.923567	0.739796	4309	29.7172	30	23	38
1	6	132	477.543	342.586	116	1.10393	0.423593	12.153	0.913386	0.74359	4237	36.5259	39	30	43
1	6	133	479.45	22.1651	109	1.42045	0.710199	11.7806	0.923729	0.778571	4270	39.1743	40	31	48
1	6	134	485.604	60.2073	164	2.07652	0.876405	14.4503	0.916201	0.780952	5044	30.7561	33	25	37
1	6	135	480.397	168.905	63	1.41513	0.707564	8.95623	0.851351	0.63	6763	107.349	109	85	134
1	6	136	490.58	254.707	174	1.55756	0.766678	14.8843	0.935484	0.74359	6842	39.3218	41	31	47
1	6	137	487.806	313.887	62	1.60841	0.783231	8.88487	0.898551	0.805195	3893	62.7903	65	51	75
1	6	138	496.029	331.5	208	2.09048	0.878165	16.2737	0.822134	0.521303	8882	42.7019	43	32	53
1	6	139	498.219	7.92708	96	1.10594	0.427089	11.0558	0.90566	0.727273	4030	41.9792	44	33	50
1	6	140	498.817	358.104	115	1.19899	0.551714	12.1005	0.942623	0.804196	4250	36.9565	38	29	44
1	6	141	501.108	502.892	93	1.00155	0.0555964	10.8817	0.920792	0.768595	3878	41.6989	42	32	50
1	7	1	13.1717	58.4545	99	1.42754	0.713646	11.2272	0.891892	0.707143	3940	39.798	40	32	48
1	7	2	22.2857	68.4388	98	1.39204	0.695662	11.1704	0.890909	0.7	3938	40.1837	42	32	47
1	7	3	24.3438	345.156	96	1.19415	0.54657	11.0558	0.923077	0.727273	4129	43.0104	44	34	53
1	7	4	31.2399	23.5351	271	1.67369	0.801881	18.5755	0.783237	0.654589	8489	31.3247	32	24	39
1	7	5	27.97	130.52	100	1.30965	0.645736	11.2838	0.925926	0.769231	4244	42.44	44	34	51
1	7	6	30.458	144.626	131	1.82018	0.835562	12.9149	0.903448	0.727778	5658	43.1908	44	34	52
1	7	7	30.0086	486.681	116	1.49932	0.745087	12.153	0.913386	0.686391	4109	35.4224	37	28	43
1	7	8	38.7195	195.928	221	1.71096	0.811418	16.7746	0.928571	0.701587	5177	23.4253	24	18	29
1	7	9	35.513	379.287	115	1.15651	0.502344	12.1005	0.905512	0.737179	4277	37.1913	38	29	46
1	7	10	35.7714	414.6	35	1.37755	0.687772	6.67558	0.897436	0.729167	5404	154.4	164	120	194
1	7	11	46.23	272.97	100	1.08978	0.397477	11.2838	0.917431	0.757576	4182	41.82	43	34	50
1	7	12	49.9759	76.6747	166	1.23086	0.583048	14.5381	0.917127	0.741071	8273	49.8373	51	40	59
1	7	13	49.7219	137.887	151	1.48031	0.737328	13.8658	0.920732	0.719048	5049	33.4371	35	26	40
1	7	14	53.4902	91.1242	153	1.67967	0.803464	13.9573	0.910714	0.772727	8574	56.0392	58	44	67
1	7	15	58.2083	30.3333	96	1.56263	0.768419	11.0558	0.897196	0.666667	3591	37.4063	40	30	45
1	7	16	66.7215	223.744	219	1.88308	0.847343	16.6985	0.939914	0.711039	4999	22.8265	24	18	28
1	7	17	68.2202	489.917	109	1.93494	0.8561	11.7806	0.872	0.605556	4065	37.2936	38	28	47
1	7	18	77.1481	261.287	108	1.46834	0.732245	11.7265	0.915254	0.72	4321	40.0093	42	33	49
1	7	19	79.8741	132.719	135	1.65215	0.796019	13.1106	0.9	0.642857	4592	34.0148	36	26	42
1	7	20	79.1333	311.013	75	1.25902	0.60757	9.77205	0.914634	0.757576	3898	51.9733	53	42	62
1	7	21	79.1449	422.848	138	1.26926	0.61585	13.2555	0.926174	0.766667	4437	32.1522	33	25	39
1	7	22	86.9679	277.058	156	2.24154	0.894972	14.0935	0.928571	0.825397	4699	30.1218	31	23	37
1	7	23	85.8039	368.268	153	1.70677	0.810381	13.9573	0.916168	0.732057	4526	29.5817	30	23	37
1	7	24	91.7971	43.0638	345	1.77297	0.825758	20.9587	0.8625	0.709877	13087	37.9333	39	30	46
1	7	25	88.3014	327.219	73	1.28553	0.628398	9.64088	0.935897	0.737374	3957	54.2055	55	43	65
1	7	26	95.0667	101.005	195	1.76841	0.824763	15.757	0.942029	0.77381	9668	49.5795	52	41	60
1	7	27	94.8161	187.977	174	1.5115	0.749861	14.8843	0.95082	0.78733	4673	26.8563	28	21	33
1	7	28	95.9318	388	132	1.57466	0.772463	12.9641	0.891892	0.628571	4467	33.8409	35	26	41
1	7	29	96.8947	297.728	114	1.38869	0.693866	12.0478	0.897638	0.74026	4079	35.7807	36	28	44
1	7	30	104.784	86.024	167	2.0048	0.866715	14.5819	0.922652	0.722944	9204	55.1138	57	43	66
1	7	31	100.91	242.72	100	1.33022	0.659442	11.2838	0.917431	0.769231	4252	42.52	43	33	51
1	7	32	105.849	492.497	159	1.88554	0.847777	14.2283	0.903409	0.679487	4668	29.3585	30	23	36
1	7	33	108.051	141.037	136	1.77383	0.825944	13.159	0.918919	0.8	4218	31.0147	31	23	38
1	7	34	114.5	219.5	148	1.5001	0.745397	13.7273	0.91358	0.660714	4563	30.8311	32	23	39
1	7	35	112.944	348.88	125	1.12674	0.46078	12.6157	0.912409	0.744048	4232	33.856	34	27	41
1	7	36	122.696	389.301	359	2.25958	0.896739	21.3797	0.8975	0.543939	21578	60.1058	60	43	76
1	7	37	118.715	407.016	123	1.96567	0.860924	12.5143	0.911111	0.585714	4530	36.8293	38	29	45
1	7	38	125.698	131.671	149	1.82258	0.836038	13.7736	0.908537	0.712919	4391	29.4698	30	23	36
1	7	39	127.937	335.779	190	1.73451	0.817074	15.5536	0.892019	0.695971	4777	25.1421	26	20	31
1	7	40	129.657	289.657	105	1.29891	0.638191	11.5624	0.913043	0.729167	3997	38.0667	40	29	47

1	7	41	132.831	416.085	118	1.57941	0.77403	12.2573	0.929134	0.7375	4370	37.0339	39	29	44
1	7	42	141.089	179.484	192	1.86987	0.844981	15.6353	0.91866	0.627451	4755	24.7656	25	19	31
1	7	43	146.275	477.265	298	1.81175	0.833875	19.4788	0.823204	0.525573	9510	31.9128	33	25	39
1	7	44	145.752	312.468	141	1.1543	0.499474	13.3988	0.915584	0.723077	4314	30.5957	32	24	37
1	7	45	148.67	36.2611	203	1.35381	0.674085	16.0769	0.944186	0.763158	9182	45.2315	47	35	55
1	7	46	151.921	219.534	189	1.68964	0.806053	15.5126	0.935644	0.75	4903	25.9418	26	20	32
1	7	47	150.379	93.6746	169	1.91984	0.853632	14.6689	0.923497	0.670635	4649	27.5089	28	21	34
1	7	48	155.872	245.497	187	2.03862	0.871425	15.4304	0.921182	0.636054	7571	40.4866	42	31	49
1	7	49	155.578	139.748	135	1.54998	0.76404	13.1106	0.912162	0.767045	4292	31.7926	33	25	39
1	7	50	164.323	388.369	198	2.46046	0.913683	15.8777	0.92093	0.6875	5235	26.4394	27	20	32
1	7	51	177.089	501.03	336	3.04299	0.944461	20.6835	0.835821	0.738462	9838	29.2798	31	21	37
1	7	52	175.35	180.975	160	1.74376	0.819225	14.273	0.91954	0.683761	4476	27.975	29	22	34
1	7	53	182.463	312.893	177	2.06497	0.874919	15.0121	0.907692	0.578431	6096	34.4407	36	27	41
1	7	54	182.062	31.9482	193	1.13599	0.474432	15.6759	0.881279	0.709559	8459	43.829	44	34	53
1	7	55	183.867	145.944	143	1.68217	0.804117	13.4935	0.899371	0.647059	4328	30.2657	31	24	37
1	7	56	183.435	436.351	131	1.32047	0.653061	12.9149	0.935714	0.779762	4343	33.1527	34	26	39
1	7	57	191.742	254.049	388	1.6823	0.804152	22.2265	0.864143	0.646667	19335	49.8325	52	39	60
1	7	58	187.664	466.48	152	1.63697	0.791721	13.9116	0.921212	0.745098	4421	29.0855	30	22	36
1	7	59	191.774	354.361	208	2.11997	0.881757	16.2737	0.920354	0.630303	8950	43.0288	44	33	52
1	7	60	199.537	34.8299	147	2.09237	0.8784	13.6809	0.924528	0.6125	4256	28.9524	30	23	34
1	7	61	199.765	391.686	226	1.16339	0.511034	16.9633	0.933884	0.738562	8913	39.4381	42	30	49
1	7	62	202.694	117.496	121	1.8066	0.832832	12.4122	0.883212	0.647059	4298	35.5207	37	27	44
1	7	63	223.218	472.545	156	1.52289	0.754197	14.0935	0.906977	0.696429	4265	27.3397	28	21	33
1	7	64	223.645	75.8455	110	1.67258	0.801587	11.8345	0.92437	0.733333	6320	57.4545	61	46	69
1	7	65	225.35	212.617	206	1.72215	0.814138	16.1953	0.923767	0.754579	4394	21.3301	22	16	27
1	7	66	230.35	311.387	160	2.02402	0.869424	14.273	0.930233	0.8	7553	47.2062	50	37	57
1	7	67	229.214	47.3761	117	1.78922	0.829234	12.2053	0.9	0.664773	6538	55.8803	59	44	67
1	7	68	230.252	426.811	143	1.50452	0.747143	13.4935	0.916667	0.680952	4484	31.3566	32	23	39
1	7	69	233.37	135.378	127	1.19809	0.550763	12.7162	0.92029	0.755952	4349	34.2441	35	26	42
1	7	70	239.567	368.239	180	1.3281	0.658072	15.1388	0.923077	0.703125	9241	51.3389	53	40	64
1	7	71	245.531	256.523	243	1.81026	0.833575	17.5897	0.94186	0.778846	5636	23.1934	24	18	28
1	7	72	246.538	393.9	130	1.66474	0.799479	12.8655	0.921986	0.666667	4446	34.2	35	26	43
1	7	73	254.628	478.726	317	1.58668	0.776396	20.0902	0.878116	0.600379	14100	44.4795	44	32	57
1	7	74	251.756	330.701	127	1.50066	0.745619	12.7162	0.913669	0.647959	4629	36.4488	37	29	45
1	7	75	260.117	438.662	145	2.16787	0.887254	13.5875	0.895062	0.635965	4313	29.7448	30	24	37
1	7	76	272.667	226.453	285	2.07848	0.876654	19.0492	0.92233	0.633333	7294	25.593	26	20	31
1	7	77	271.121	89.2349	149	1.58153	0.774724	13.7736	0.91411	0.674208	4396	29.5034	30	22	37
1	7	78	271.065	418.276	123	1.4177	0.70884	12.5143	0.938931	0.727811	4288	34.8618	37	28	41
1	7	79	275.814	457.496	129	1.19877	0.551482	12.8159	0.902098	0.708791	4334	33.5969	35	26	41
1	7	80	281.035	107.674	144	1.36406	0.680115	13.5406	0.941176	0.8	4390	30.4861	32	23	36
1	7	81	283.372	378.194	180	1.37189	0.684597	15.1388	0.932642	0.75	8558	47.5444	49	37	59
1	7	82	291.019	305.957	208	1.55843	0.766981	16.2737	0.924444	0.742857	9450	45.4327	48	35	56
1	7	83	291.844	425.593	135	1.92398	0.854314	13.1106	0.944056	0.833333	4238	31.3926	32	25	38
1	7	84	302.061	495.628	164	1.18633	0.538012	14.4503	0.906077	0.689076	5496	33.5122	35	25	42
1	7	85	326.196	440.576	715	2.71841	0.929881	30.1723	0.657169	0.383996	20112	28.1287	29	21	35
1	7	86	318.028	379.6	180	1.80836	0.833189	15.1388	0.909091	0.625	8018	44.5444	46	34	55
1	7	87	319.139	480.525	122	1.19159	0.543796	12.4634	0.903704	0.72619	4028	33.0164	35	27	39
1	7	88	327.788	397.964	165	1.73598	0.817419	14.4943	0.901639	0.654762	4706	28.5212	30	23	34
1	7	89	338.806	170.942	191	2.02727	0.869874	15.5945	0.896714	0.606349	8694	45.5183	48	37	54
1	7	90	344.676	379.211	71	1.67896	0.803276	9.50789	0.910256	0.739583	4011	56.493	57	46	69
1	7	91	353.418	364.282	213	2.08045	0.876904	16.4682	0.918103	0.591667	8798	41.3052	42	32	50
1	7	92	362.19	94.9241	158	1.5969	0.779653	14.1835	0.913295	0.663866	4870	30.8228	32	24	38
1	7	93	362.172	330.46	87	1.04982	0.304404	10.5248	0.915789	0.719008	3703	42.5632	44	35	52
1	7	94	361.328	388.148	61	1.41465	0.707325	8.81292	0.884058	0.7625	3820	62.623	64	51	76
1	7	95	377.571	322.073	259	1.66998	0.800892	18.1595	0.863333	0.6475	13664	52.7568	51	39	67
1	7	96	380.455	482.961	231	2.67939	0.927743	17.1499	0.916667	0.712963	5820	25.1948	26	19	31
1	7	97	383.223	355.843	121	1.30452	0.642169	12.4122	0.916667	0.733333	4088	33.7851	34	27	41
1	7	98	398.118	460.118	161	2.14008	0.884113	14.3175	0.909605	0.557093	5244	32.5714	34	26	39
1	7	99	395.224	337.158	76	1.55327	0.765192	9.83698	0.904762	0.730769	3878	51.0263	53	40	62
1	7	100	400.468	234.995	203	1.63778	0.791954	16.0769	0.922727	0.667763	8751	43.1084	45	32	55
1	7	101	403.29	274.575	193	1.85043	0.841399	15.6759	0.923445	0.630719	6950	36.0104	37	27	44
1	7	102	405.127	381.542	142	1.23011	0.582352	13.4462	0.922078	0.728205	4346	30.6056	32	23	37
1	7	103	416.389	360.643	126	1.31237	0.647598	12.666	0.913043	0.75	4165	33.0556	34	26	40
1	7	104	423.782	433.085	436	1.8334	0.838154	23.5612	0.872	0.619318	18633	42.7362	44	33	53
1	7	105	429.267	58.6533	150	1.28378	0.627084	13.8198	0.931677	0.78125	4218	28.12	29	22	34
1	7	106	437.237	209.237	38	1.71276	0.811859	6.9558	0.826087	0.59375	3012	79.2632	80	61	100
1	7	107	442.343	200.857	35	1.44058	0.719817	6.67558	0.875	0.729167	2872	82.0571	82	60	100
1	7	108	460.931	222.448	174	1.75735	0.82231	14.8843	0.935484	0.790909	5908	33.954	35	27	40
1	7	109	463.61	277.99	105	1.78648	0.828655	11.5624	0.897436	0.625	3901	37.1524	38	30	46
1	7	110	466.516	321.648	122	1.41784	0.708913	12.4634	0.917293	0.72619	4585	37.582	39	30	45
1	7	111	473.647	121.924	119	1.70559	0.810088	12.3092	0.868613	0.610256	3984	33.479	35	26	40
1	7	112	482.816	335.798	114	1.13184	0.468399	12.0478	0.934426	0.797203	4228	37.0877	39	29	44
1	7	113	486.5	287.192	104	1.15544	0.500955	11.5073	0.896552	0.727273	3893	37.4327	39	29	45
1	7	114	497.774	121.27	115	1.44336	0.721103	12.1005	0.891473	0.69697	3920	34.087	35	27	41
1	7	115	499.638	314.244	127	1.47025	0.733067	12.7162	0.913669	0.705556	4436	34.9291	37	28	41
1	7	116	502.026	136.756	156	1.15883	0.505312	14.0935	0.939759	0.8	4744	30.4103	32	23	37

1	8	1	11.1154	387.587	104	1.42586	0.712837	11.5073	0.904348	0.675325	3955	38.0288	39	31	46		
1	8	2	9.80303	429.712	66	1.2069	0.559891	9.167	0.88	0.733333	3059	46.3485	48	40	53		
1	8	3	11.6364	443.818	77	1.17652	0.526846	9.90149	0.927711	0.77	2990	38.8312	40	34	44		
1	8	4	14.4143	456.586	70	1.03328	0.251744	9.4407	0.886076	0.7	3970	56.7143	58	46	68		
1	8	5	18.3947	45.1316	114	1.263	0.610824	12.0478	0.912	0.730769	3892	34.1404	35	27	41		
1	8	6	21.18	172.58	100	1.52012	0.753156	11.2838	0.884956	0.714286	3840	38.4	39	31	47		
1	8	7	25.1143	499.143	140	1.52652	0.755554	13.3512	0.903226	0.673077	4072	29.0857	30	22	36		
1	8	8	25.8148	433.905	189	1.95543	0.859345	15.5126	0.836283	0.63	12608	66.709	69	51	84		
1	8	9	25.8947	150.614	114	1.27031	0.616685	12.0478	0.919355	0.730769	4004	35.1228	37	28	43		
1	8	10	27.688	113.544	125	1.44333	0.721089	12.6157	0.905797	0.694444	7138	57.104	60	44	69		
1	8	11	27.9023	349.684	133	1.23456	0.58642	13.0131	0.917241	0.738889	4208	31.6391	32	25	39		
1	8	12	28.6991	66.8407	113	1.33116	0.660045	11.9948	0.91129	0.724359	4075	36.0619	37	29	44		
1	8	13	30.7857	380.439	196	1.80157	0.831803	15.7973	0.903226	0.606811	5557	28.352	30	22	35		
1	8	14	36.7762	311.455	143	1.07869	0.374947	13.4935	0.922581	0.785714	4063	28.4126	29	23	34		
1	8	15	49.0119	37.619	252	1.38906	0.694066	17.9125	0.82623	0.572727	11427	45.3452	45	34	58		
1	8	16	45.7623	123.623	122	1.10508	0.425606	12.4634	0.917293	0.782051	4662	38.2131	39	30	46		
1	8	17	46.7836	203.731	134	1.60438	0.781987	13.0619	0.937063	0.683673	4152	30.9851	32	25	37		
1	8	18	50.717	68.5566	212	1.49816	0.744624	16.4294	0.917749	0.69281	8804	41.5283	42	32	52		
1	8	19	53.3043	461.739	92	1.44718	0.722855	10.823	0.910891	0.69697	3641	39.5761	39	31	49		
1	8	20	66.0732	162.192	478	1.03578	0.260563	24.67	0.910476	0.735385	14880	31.1297	32	24	38		
1	8	21	64.6333	121.808	120	1.21481	0.567792	12.3608	0.895522	0.710059	4070	33.9167	35	27	41		
1	8	22	68.3801	270.181	221	1.5985	0.780155	16.7746	0.936441	0.736667	7891	35.7059	37	28	43		
1	8	23	64.7756	339.558	156	1.54808	0.763371	14.0935	0.923077	0.787879	4298	27.5513	28	21	34		
1	8	24	66.2917	50.0764	144	2.23108	0.893926	13.5406	0.947368	0.8	5206	36.1528	37	28	44		
1	8	25	67.2043	473	93	1.33433	0.662074	10.8817	0.902913	0.65035	3739	40.2043	41	33	49		
1	8	26	72.6838	297.915	117	1.44204	0.720491	12.2053	0.906977	0.709091	3961	33.8547	34	26	41		
1	8	27	72.582	401.974	189	2.01167	0.867693	15.5126	0.917476	0.642857	5541	29.3175	30	23	36		
1	8	28	76.6716	134.731	134	1.70384	0.809651	13.0619	0.911565	0.697917	4152	30.9851	33	24	37		
1	8	29	74.6636	109.168	107	1.23867	0.590113	11.672	0.90678	0.748252	4122	38.5234	39	30	47		
1	8	30	85.2585	188.102	147	2.37263	0.906841	13.6809	0.90184	0.668182	4231	28.7823	29	23	36		
1	8	31	84.292	74.7611	113	1.16561	0.513778	11.9948	0.904	0.724359	4168	36.885	38	29	46		
1	8	32	95.8089	208.6	403	1.49429	0.743068	22.6521	0.846639	0.648953	14872	36.9032	37	28	45		
1	8	33	90.5596	140.101	109	1.57451	0.772416	11.7806	0.893443	0.64881	4053	37.1835	39	30	45		
1	8	34	98.5458	463.579	273	1.91669	0.853109	18.6439	0.877814	0.598684	13955	51.1172	52	38	64		
1	8	35	99.1137	247.933	299	1.62483	0.788176	19.5115	0.937304	0.684211	9570	32.0067	33	25	39		
1	8	36	98.2744	37.556	277	2.98601	0.942255	18.78	0.882166	0.502722	7730	27.9061	29	21	34		
1	8	37	98.7634	166.452	93	1.67096	0.801153	10.8817	0.885714	0.65035	3856	41.4624	42	32	50		
1	8	38	108.512	493.449	205	2.13682	0.883736	16.1559	0.911111	0.711806	4628	22.5756	23	17	28		
1	8	39	112.24	441.98	150	1.6123	0.784417	13.8198	0.931677	0.757576	7793	51.9533	53	40	64		
1	8	40	111.812	222.761	117	1.95283	0.85894	12.2053	0.906977	0.764706	4458	38.1026	39	31	45		
1	8	41	113.866	346.631	149	1.39804	0.698828	13.7736	0.91411	0.716346	4233	28.4094	30	21	34		
1	8	42	120.83	411.358	106	1.31794	0.65137	11.6174	0.929825	0.815385	3923	37.0094	37	29	45		
1	8	43	129.929	192.143	84	1.15603	0.50172	10.3418	0.903226	0.694215	2693	32.0595	33	25	38		
1	8	44	137.19	454.365	252	1.89597	0.849596	17.9125	0.854237	0.672	9387	37.25	38	28	46		
1	8	45	134.843	128.974	305	2.06323	0.874693	19.7063	0.918675	0.680804	8280	27.1475	28	21	34		
1	8	46	141.141	215.84	319	1.50812	0.748552	20.1535	0.932749	0.693478	11477	35.9781	36	28	43		
1	8	47	137.059	242.798	119	1.33313	0.661311	12.3092	0.915385	0.772727	3584	30.1176	31	24	36		
1	8	48	145.367	17.8986	207	1.77589	0.82639	16.2345	0.924107	0.704082	8582	41.4589	44	32	50		
1	8	49	153.278	413.183	115	1.65246	0.796105	12.1005	0.927419	0.680473	4040	35.1304	37	28	42		
1	8	50	159.463	278.456	136	1.06378	0.341056	13.159	0.937931	0.747253	4230	31.1029	33	25	37		
1	8	51	159.706	91.2327	245	2.00944	0.867377	17.6619	0.924528	0.753846	8913	36.3796	37	28	44		
1	8	52	159.59	393.024	83	1.4086	0.70428	10.28	0.912088	0.691667	3838	46.241	47	37	57		
1	8	53	164.983	500.36	175	1.69183	0.806617	14.9271	0.91623	0.643382	4480	25.6	26	20	31		
1	8	54	170.853	257.131	375	1.34636	0.669575	21.851	0.910194	0.708885	14547	38.792	39	31	48		
1	8	55	177.162	54.2575	167	1.52019	0.753181	14.5819	0.912568	0.701681	5095	30.509	32	24	36		
1	8	56	178.6	387.358	95	1.20724	0.560236	10.9981	0.896226	0.719697	3826	40.2737	40	32	49		
1	8	57	182.152	435.777	224	2.7007	0.928922	16.888	0.858238	0.518519	9007	40.2098	40	31	51		
1	8	58	179.327	459.119	101	1.22641	0.578918	11.3401	0.926606	0.765152	4011	39.7129	41	33	48		
1	8	59	183.359	190.781	128	1.23747	0.589043	12.7662	0.948148	0.820513	2772	21.6563	22	17	26		
1	8	60	185.464	503.145	110	1.86455	0.844013	11.8345	0.887097	0.604396	4156	37.7818	39	29	47		
1	8	61	197.076	139.323	223	1.63285	0.790527	16.8503	0.940928	0.724026	8777	39.3587	39	30	50		
1	8	62	194.681	214.072	138	2.23437	0.894257	13.2555	0.907895	0.766667	4036	29.2464	30	22	36		
1	8	63	199.681	455.08	113	1.71204	0.811602	11.9948	0.91129	0.684848	4036	35.7168	36	27	44		
1	8	64	207.119	282.204	226	1.93002	0.855302	16.9633	0.896825	0.724359	7754	34.3097	36	27	41		
1	8	65	203.444	35.0171	117	1.26158	0.609669	12.2053	0.92126	0.75974	3975	33.9744	35	26	42		
1	8	66	206.23	259.208	178	1.36462	0.680437	15.0545	0.92228	0.706349	6679	37.5225	39	30	46		
1	8	67	210.406	15.8125	128	1.45902	0.728174	12.7662	0.901408	0.711111	4017	31.3828	32	24	39		
1	8	68	220.184	93.6399	461	1.13472	0.472599	24.2273	0.931313	0.770903	18442	40.0043	42	30	50		
1	8	69	225.178	214.767	163	1.11492	0.44218	14.4062	0.926136	0.724444	4374	26.8344	28	21	33		
1	8	70	230.979	235.904	146	1.31912	0.65216	13.6343	0.918239	0.695238	4134	28.3151	29	22	35		
1	8	71	236.673	495.272	346	2.33131	0.903331	20.9891	0.800926	0.518741	10802	31.2197	33	23	39		
1	8	72	235.502	132.659	255	1.7484	0.820288	18.0188	0.897887	0.643939	8918	34.9725	36	27	42		
1	8	73	231.124	391.719	89	1.45186	0.724978	10.6451	0.89899	0.760684	4314	48.4719	47	38	59		
1	8	74	242.741	156.606	251	2.26019	0.896797	17.8769	0.820261	0.603365	9132	36.3825	38	28	45		
1	8	75	239.34	189.296	162	1.7497	0.820584	14.3619	0.89011	0.692308	4184	25.8272	26	20	31		
1	8	76	238.514	24.8551	138	1.77073	0.825269	13.2555	0.92	0.657143	4080	29.5652	30	23	36		

1	8	77	241.36	45.3128	211	1.69785	0.808148	16.3907	0.946188	0.753571	8135	38.5545	40	30	47
1	8	78	241.66	308.241	191	1.60919	0.783469	15.5945	0.927184	0.773279	4521	23.6702	25	18	29
1	8	79	249.134	425.698	149	1.63414	0.790903	13.7736	0.93125	0.716346	4359	29.255	30	22	36
1	8	80	248.37	378.26	73	1.24745	0.597815	9.64088	0.890244	0.675926	3060	41.9178	43	35	51
1	8	81	248.378	398.218	156	2.20066	0.890793	14.0935	0.852459	0.6	9763	62.5833	59	47	80
1	8	82	259.588	266.39	182	1.84198	0.839801	15.2227	0.896552	0.594771	4283	23.533	25	19	29
1	8	83	273.394	203.522	251	2.33573	0.903716	17.8769	0.831126	0.518595	9000	35.8566	37	26	46
1	8	84	273.527	441.305	131	2.15733	0.886078	12.9149	0.89726	0.661616	4492	34.2901	34	26	42
1	8	85	273.769	485.615	143	1.38607	0.692449	13.4935	0.928571	0.744792	4196	29.3427	31	23	35
1	8	86	278.037	162.951	268	1.50594	0.7477	18.4724	0.930556	0.708995	8918	33.2761	35	26	40
1	8	87	278.313	457.267	150	1.60585	0.782443	13.8198	0.898204	0.694444	4322	28.8133	29	23	36
1	8	88	282.808	48.0113	177	1.13131	0.467621	15.0121	0.941489	0.786667	4236	23.9322	25	20	28
1	8	89	292.118	64	170	1.75669	0.822163	14.7123	0.918919	0.772727	4143	24.3706	26	19	29
1	8	90	293.917	412.439	132	1.32413	0.655479	12.9641	0.916667	0.733333	6542	49.5606	50	39	60
1	8	91	300.819	214.943	105	1.43507	0.717238	11.5624	0.905172	0.673077	3901	37.1524	39	30	45
1	8	92	301.375	365.235	136	1.35237	0.673221	13.159	0.931507	0.747253	7767	57.1103	59	46	69
1	8	93	305.595	44.2727	264	1.97196	0.861881	18.334	0.778761	0.597285	8734	33.0833	34	26	40
1	8	94	309.638	83.3276	116	1.25302	0.602565	12.153	0.899225	0.637363	6893	59.4224	61	47	73
1	8	95	311.872	109.156	179	1.46636	0.73139	15.0967	0.927461	0.724696	6657	37.1899	38	28	46
1	8	96	319.228	247.71	272	1.72353	0.814471	18.6097	0.874598	0.618182	9264	34.0588	35	26	42
1	8	97	320.663	479.596	312	1.59325	0.778498	19.9311	0.891429	0.619048	18606	59.6346	62	47	72
1	8	98	323.679	199.77	296	1.77625	0.826468	19.4134	0.87574	0.770833	9457	31.9493	33	26	38
1	8	99	328.266	156.173	335	1.62631	0.788615	20.6527	0.856777	0.744444	14483	43.2328	44	33	53
1	8	100	324.84	416.43	244	2.40222	0.909235	17.6258	0.893773	0.625641	9558	39.1721	41	30	47
1	8	101	329.622	216.832	119	1.69567	0.807594	12.3092	0.901515	0.653846	4050	34.0336	35	27	41
1	8	102	332.686	380.265	102	1.34389	0.668061	11.3961	0.910714	0.728571	3971	38.9314	40	30	47
1	8	103	340.491	119.604	106	1.12248	0.454237	11.6174	0.921739	0.736111	4013	37.8585	39	30	46
1	8	104	348.5	136.445	110	1.50007	0.745305	11.8345	0.901639	0.654762	4017	36.5182	38	28	44
1	8	105	347.429	366.747	91	1.99171	0.864821	10.7641	0.919192	0.631944	3658	40.1978	41	31	50
1	8	106	348.818	238.455	121	1.14875	0.492147	12.4122	0.923664	0.775641	4263	35.2314	37	27	43
1	8	107	352.032	268.525	158	1.65609	0.797113	14.1835	0.908046	0.692982	4752	30.0759	32	23	37
1	8	108	352.05	489.95	119	1.59372	0.778647	12.3092	0.929688	0.704142	4086	34.3361	35	27	41
1	8	109	352	395.853	75	1.84593	0.840551	9.77205	0.882353	0.641026	3532	47.0933	49	36	60
1	8	110	354.868	111.082	182	1.68499	0.804853	15.2227	0.928571	0.736842	7726	42.4505	44	33	51
1	8	111	360.267	337.283	180	1.12392	0.456455	15.1388	0.927835	0.75	8844	49.1333	52	39	59
1	8	112	360.8	294.429	105	1.37302	0.685237	11.5624	0.9375	0.807692	3915	37.2857	37	29	45
1	8	113	360.621	184.388	116	1.47774	0.736252	12.153	0.885496	0.70303	3985	34.3534	36	27	41
1	8	114	368.133	45.8833	180	1.3587	0.676984	15.1388	0.918367	0.666667	4291	23.8389	24	18	29
1	8	115	362.3	432.778	90	1.68704	0.805383	10.7047	0.909091	0.75	3718	41.3111	42	32	52
1	8	116	365.721	494.077	104	1.52379	0.754535	11.5073	0.912281	0.693333	3903	37.5288	38	31	44
1	8	117	368.154	314.396	91	1.31092	0.646607	10.7641	0.91	0.758333	3794	41.6923	42	33	51
1	8	118	372.21	175.807	119	1.36563	0.68102	12.3092	0.901515	0.708333	4159	34.9496	36	27	43
1	8	119	373.35	213.65	143	1.0509	0.30746	13.4935	0.916667	0.729592	4415	30.8741	33	24	38
1	8	120	374.943	76.1478	230	2.12981	0.882919	17.1127	0.855019	0.613333	8527	37.0739	38	29	46
1	8	121	379.519	247.099	131	1.34195	0.666857	12.9149	0.922535	0.71978	4452	33.9847	36	28	40
1	8	122	385.722	277	115	1.19258	0.544875	12.1005	0.927419	0.804196	4175	36.3043	38	30	43
1	8	123	389.102	93.1497	167	1.2864	0.629051	14.5819	0.932961	0.755656	8366	50.0958	52	39	60
1	8	124	394.136	163.603	184	1.22361	0.576281	15.3061	0.938776	0.773109	8747	47.538	50	37	57
1	8	125	401.325	17.596	302	2.38349	0.907731	19.6091	0.883041	0.719048	17267	57.1755	58	44	70
1	8	126	398.503	250.074	312	2.69457	0.928586	19.9311	0.850136	0.484472	9922	31.8013	33	25	39
1	8	127	398.398	394.667	93	1.43899	0.719074	10.8817	0.894231	0.715385	3854	41.4409	42	32	51
1	8	128	408.33	139.141	227	2.83374	0.935664	17.0007	0.886719	0.493478	4413	19.4405	19	15	25
1	8	129	417.863	122.789	175	1.49851	0.744764	14.9271	0.935829	0.747863	4396	25.12	26	20	31
1	8	130	419.559	405.314	102	1.13504	0.473065	11.3961	0.910714	0.708333	4035	39.5588	41	30	48
1	8	131	445.338	198.923	234	1.84451	0.840283	17.2609	0.947368	0.782609	9125	38.9957	41	31	47
1	8	132	441.946	88.2473	186	1.56902	0.777149	15.389	0.925373	0.775	8002	43.0215	46	34	51
1	8	133	447.858	270.362	127	1.23599	0.587712	12.7162	0.927007	0.751479	3960	31.1811	33	25	38
1	8	134	447.276	30.0789	76	1.12741	0.461785	9.83698	0.873563	0.690909	3362	44.2368	46	36	55
1	8	135	451.223	104.749	175	1.62912	0.78944	14.9271	0.925926	0.767544	7897	45.1257	47	36	54
1	8	136	451.809	422.809	110	1.31582	0.649941	11.8345	0.916667	0.705128	4025	36.5909	38	29	45
1	8	137	459.594	316.903	165	1.57515	0.772628	14.4943	0.873016	0.705128	5041	30.5515	31	24	37
1	8	138	461.477	119.946	111	1.89167	0.848851	11.8882	0.880952	0.652941	3516	31.6757	33	24	39
1	8	139	462	394	51	1.38033	0.689309	8.05824	0.910714	0.809524	7047	138.176	140	111	169
1	8	140	489.372	225.858	401	2.93477	0.940157	22.5958	0.798805	0.541161	20652	51.5012	51	39	64
1	8	141	475.079	114.763	76	1.77782	0.826805	9.83698	0.873563	0.678571	3058	40.2368	41	31	49
1	8	142	479.314	244.429	105	1.33337	0.66146	11.5624	0.897436	0.75	3522	33.5429	35	27	40
1	8	143	482.952	495.062	146	1.66638	0.799924	13.6343	0.906832	0.737374	5039	34.5137	35	27	42
1	8	144	487.34	149.102	197	1.83365	0.838202	15.8376	0.907834	0.643791	8402	42.6497	44	33	52
1	8	145	493.055	44.1978	91	1.37476	0.686216	10.7641	0.875	0.7	2990	32.8571	33	25	40
1	8	146	501.221	100.897	68	1.22476	0.577363	9.30485	0.883117	0.686869	3341	49.1324	51	39	59
1	9	1	12.1194	487.724	134	1.82898	0.837294	13.0619	0.924138	0.788235	4145	30.9328	32	24	37
1	9	2	14.3664	59.3893	131	1.71457	0.812303	12.9149	0.929078	0.770588	4166	31.8015	33	25	39
1	9	3	17.6605	303.759	162	1.46904	0.732548	14.3619	0.910112	0.680672	7203	44.463	44	35	54
1	9	4	14.3913	179.217	23	1.23546	0.58724	5.41152	0.884615	0.766667	2354	102.348	106	85	116
1	9	5	15.2593	169.593	27	1.0586	0.328094	5.86323	0.870968	0.75	2616	96.8889	97	76	123
1	9	6	24.0507	187.71	138	1.29496	0.635347	13.2555	0.926174	0.766667	5429	39.3406	41	32	48

1	9	7	21.2188	364.125	64	1.29361	0.634372	9.02703	0.876712	0.727273	3642	56.9063	57	44	68
1	9	8	24.0233	453.946	129	1.82866	0.837231	12.8159	0.921429	0.661538	3872	30.0155	30	23	37
1	9	9	35.6429	114.293	140	1.45761	0.72755	13.3512	0.909091	0.729167	4313	30.8071	31	23	38
1	9	10	39.9272	251.374	206	1.6479	0.79483	16.1953	0.919643	0.677632	9014	43.7573	45	35	53
1	9	11	38.5562	328.843	178	1.06005	0.331795	15.0545	0.927083	0.791111	9196	51.6629	52	38	64
1	9	12	39.3667	41.52	150	1.17673	0.527089	13.8198	0.920245	0.765306	4709	31.3933	33	25	38
1	9	13	38.3765	362.388	85	1.17688	0.527265	10.4031	0.894737	0.708333	3980	46.8235	49	39	57
1	9	14	45.223	24.1727	139	1.40448	0.702172	13.3034	0.958621	0.842424	4279	30.7842	32	25	36
1	9	15	57.3316	101.968	187	1.77145	0.825428	15.4304	0.912195	0.667857	4410	23.5829	24	18	29
1	9	16	55.8904	62.5274	146	1.61579	0.785475	13.6343	0.924051	0.695238	4298	29.4384	30	22	36
1	9	17	55.5476	126.373	126	1.31697	0.650718	12.666	0.9	0.692308	4098	32.5238	33	25	40
1	9	18	65.4198	170.966	324	2.47752	0.914923	20.3108	0.79803	0.482143	16200	50	52	39	61
1	9	19	61.8615	292.138	195	1.65939	0.798019	15.757	0.919811	0.714286	9025	46.2821	48	35	57
1	9	20	63.3444	214.022	180	1.7726	0.825678	15.1388	0.904523	0.714286	8730	48.5	50	37	59
1	9	21	73.2222	375.178	45	1.42858	0.714145	7.5694	0.918367	0.714286	3366	74.8	74	56	94
1	9	22	77.3137	227.052	153	1.46509	0.730839	13.9573	0.921687	0.75	4472	29.2288	30	24	35
1	9	23	76.2075	362.453	53	1.14916	0.492694	8.21472	0.913793	0.736111	3514	66.3019	69	50	80
1	9	24	83.9479	94.3646	192	1.27679	0.621756	15.6353	0.923077	0.761905	8805	45.8594	47	37	54
1	9	25	96.0609	317.826	115	1.25503	0.604248	12.1005	0.912698	0.746753	4048	35.2	36	27	43
1	9	26	98.0964	190.528	197	1.14488	0.486908	15.8376	0.920561	0.724265	9240	46.9036	48	36	59
1	9	27	96.6796	467.951	103	1.32942	0.658926	11.4518	0.895652	0.72028	4108	39.8835	41	31	49
1	9	28	102.493	121.97	203	2.8942	0.938412	16.0769	0.835391	0.461364	8738	43.0443	42	31	53
1	9	29	100.951	38.6639	122	1.72624	0.815118	12.4634	0.917293	0.622449	3920	32.1311	33	26	39
1	9	30	101.027	99.8591	149	1.86847	0.844726	13.7736	0.925466	0.662222	4349	29.1879	30	22	35
1	9	31	99.8	243.069	130	1.27609	0.621208	12.8655	0.902778	0.714286	4411	33.9308	35	27	41
1	9	32	104.422	439.385	109	1.17019	0.519347	11.7806	0.915966	0.756944	4199	38.5229	39	30	46
1	9	33	109.131	54.3367	199	1.51352	0.75064	15.9177	0.929907	0.765385	8907	44.7588	47	34	54
1	9	34	109.456	141.911	90	1.30509	0.642565	10.7047	0.918367	0.692308	3953	43.9222	45	35	53
1	9	35	110.122	343.843	115	1.22263	0.575349	12.1005	0.912698	0.746753	4134	35.9478	37	28	44
1	9	36	116.914	98.9877	81	1.22991	0.58217	10.1554	0.920455	0.818182	4046	49.9506	51	42	59
1	9	37	116.582	401.541	98	1.22722	0.57967	11.1704	0.899083	0.742424	3924	40.0408	41	33	48
1	9	38	123.37	294.65	200	1.59791	0.779969	15.9577	0.917431	0.714286	9236	46.18	47	35	58
1	9	39	128.98	131.02	99	1.28836	0.630508	11.2272	0.9	0.692308	4166	42.0808	42	33	51
1	9	40	127.437	444.757	103	1.71763	0.813046	11.4518	0.895652	0.686667	4065	39.466	41	31	48
1	9	41	133.758	196.913	277	1.47512	0.735144	18.78	0.923333	0.70844	9756	35.2202	37	26	43
1	9	42	134.911	428.693	101	1.15959	0.506271	11.3401	0.90991	0.765152	4129	40.8812	42	33	48
1	9	43	139.46	254.46	187	1.82919	0.837336	15.4304	0.916667	0.667857	9071	48.508	50	37	61
1	9	44	141.877	492	106	1.45378	0.72584	11.6174	0.929825	0.741259	4167	39.3113	40	31	48
1	9	45	146.702	221.56	84	1.39597	0.697744	10.3418	0.903226	0.777778	4112	48.9524	49	36	61
1	9	46	150	476.113	106	1.21739	0.570307	11.6174	0.898305	0.741259	4275	40.3302	42	30	49
1	9	47	161.276	449.352	105	1.38269	0.690611	11.5624	0.913043	0.681818	4157	39.5905	41	32	48
1	9	48	171.014	329.937	284	2.96996	0.94161	19.0158	0.890282	0.473333	13145	46.2852	48	36	56
1	9	49	165.614	211.861	101	1.36598	0.681225	11.3401	0.885965	0.706294	4301	42.5842	44	33	52
1	9	50	165.713	502.361	122	1.21828	0.571176	12.4634	0.910448	0.72619	4098	33.5902	35	27	41
1	9	51	169.352	42.2211	199	1.84139	0.839689	15.9177	0.921296	0.676871	8842	44.4322	46	34	54
1	9	52	182.642	191.49	349	1.96965	0.861532	21.0799	0.894872	0.606957	19671	56.3639	59	44	68
1	9	53	187.426	251.442	129	1.36425	0.680225	12.8159	0.902098	0.671875	4487	34.7829	35	28	42
1	9	54	187.183	418.358	109	1.76088	0.823099	11.7806	0.886179	0.598901	3828	35.1193	36	27	43
1	9	55	191.155	51.9	220	1.46325	0.730036	16.7366	0.932203	0.785714	8915	40.5227	41	31	50
1	9	56	192.106	128.697	142	1.35316	0.673696	13.4462	0.928105	0.728205	5924	41.7183	44	33	51
1	9	57	193.019	443.712	104	1.69636	0.807771	11.5073	0.896552	0.615385	3752	36.0769	36	28	44
1	9	58	194.321	366.037	187	2.07196	0.875821	15.4304	0.912195	0.636054	4596	24.5775	25	18	31
1	9	59	199.016	484.556	126	1.26109	0.609268	12.666	0.947368	0.807692	4126	32.746	33	25	40
1	9	60	207.261	178.63	46	1.54709	0.763022	7.65304	0.836364	0.638889	6268	136.261	142	108	166
1	9	61	209.325	373.431	160	2.41839	0.910505	14.273	0.914286	0.634921	4498	28.1125	28	21	36
1	9	62	214.169	59.5135	148	1.79868	0.831208	13.7273	0.89697	0.685185	4687	31.6689	33	25	38
1	9	63	217.664	231.645	152	1.81213	0.833953	13.9116	0.926829	0.8	4545	29.9013	31	23	36
1	9	64	219.311	73.4662	148	1.62943	0.78953	13.7273	0.942675	0.791444	6274	42.3919	43	33	51
1	9	65	222.944	99.6111	144	1.47822	0.736453	13.5406	0.917197	0.705882	4420	30.6944	32	24	37
1	9	66	222.402	498.069	102	1.44952	0.723919	11.3961	0.894737	0.662338	3850	37.7451	39	30	47
1	9	67	227.369	450.393	84	1.22251	0.57523	10.3418	0.933333	0.763636	3723	44.3214	46	36	53
1	9	68	232.114	280.992	123	1.40951	0.704741	12.5143	0.924812	0.745455	4194	34.0976	35	26	42
1	9	69	235.639	393.325	166	2.34611	0.904612	14.5381	0.907104	0.542484	4447	26.7892	27	20	33
1	9	70	234.904	159.211	209	1.50663	0.747971	16.3128	0.93722	0.765568	9114	43.6077	46	35	54
1	9	71	236.104	297.94	134	1.48761	0.740352	13.0619	0.911565	0.761364	4302	32.1045	33	25	39
1	9	72	237.048	27.3942	104	1.59005	0.777477	11.5073	0.912281	0.693333	3989	38.3558	40	31	47
1	9	73	242.184	51.7053	207	1.81456	0.83444	16.2345	0.907895	0.723776	7036	33.9903	33	25	43
1	9	74	242.764	78.9857	140	1.39685	0.698205	13.3512	0.903226	0.666667	4272	30.5143	31	23	38
1	9	75	245.917	439.287	108	1.58813	0.776862	11.7265	0.931034	0.8	4021	37.2315	38	29	45
1	9	76	252.39	397.256	172	1.71191	0.811652	14.7986	0.900524	0.646617	4653	27.0523	28	21	33
1	9	77	265.139	261.344	294	1.5947	0.778957	19.3477	0.88024	0.665158	9550	32.483	34	24	40
1	9	78	267.579	39.9331	254	1.38602	0.692424	17.9834	0.852349	0.711485	9097	35.815	35	27	43
1	9	79	276.18	118.626	278	1.33653	0.663466	18.8138	0.905537	0.661905	16009	57.5863	60	43	71
1	9	80	277.402	11.082	122	1.34993	0.671749	12.4634	0.924242	0.72619	4199	34.418	36	28	41
1	9	81	285.594	491.97	298	1.62601	0.788526	19.4788	0.814208	0.580897	9476	31.7987	33	24	39
1	9	82	287.241	474.126	278	2.44737	0.912713	18.8138	0.810496	0.620536	9278	33.3741	34	26	40

1	9	83	283.646	101.811	127	1.6886	0.805787	12.7162	0.913669	0.661458	4625	36.4173	37	29	44
1	9	84	284.665	440.671	173	1.53854	0.759964	14.8415	0.925134	0.758772	7670	44.3353	46	35	54
1	9	85	281.69	289.917	84	1.53454	0.758511	10.3418	0.903226	0.646154	4211	50.131	51	39	62
1	9	86	286.312	80.4481	154	1.13337	0.470646	14.0028	0.916667	0.733333	4526	29.3896	30	23	36
1	9	87	292.989	305.311	90	1.08786	0.393714	10.7047	0.909091	0.743802	4134	45.9333	46	36	56
1	9	88	300.374	47.9346	107	1.37271	0.685059	11.672	0.89916	0.764286	4067	38.0093	39	29	46
1	9	89	302.5	332.755	106	1.53544	0.758839	11.6174	0.938053	0.84127	4700	44.3396	44	36	54
1	9	90	310.561	348.784	148	2.38785	0.908085	13.7273	0.840909	0.528571	8947	60.4527	60	41	74
1	9	91	305.159	364.341	44	1.29753	0.637205	7.48482	0.846154	0.6875	3760	85.4545	88	65	106
1	9	92	313.183	388.246	224	2.05865	0.874094	16.888	0.914286	0.59893	9246	41.2768	43	32	50
1	9	93	312.337	242.253	359	2.13587	0.883626	21.3797	0.810384	0.569841	19817	55.2006	56	42	69
1	9	94	315.082	322.148	182	1.48417	0.738934	15.2227	0.928571	0.736842	9474	52.0549	55	41	64
1	9	95	322.65	51.4724	163	1.82189	0.835902	14.4062	0.910615	0.639216	4364	26.773	28	20	32
1	9	96	327.5	256.405	158	1.28078	0.624816	14.1835	0.923977	0.752381	4988	31.5696	33	25	38
1	9	97	343.743	422.568	241	1.64439	0.793838	17.5172	0.895911	0.634211	9916	41.1452	42	31	51
1	9	98	342.921	46.3444	151	1.33418	0.661977	13.8658	0.920732	0.725962	4249	28.1391	29	22	34
1	9	99	344.143	139.607	28	1.12668	0.460686	5.97082	0.875	0.666667	5659	202.107	215	166	238
1	9	100	352.064	283.676	173	1.60966	0.783613	14.8415	0.935135	0.758772	4699	27.1618	28	21	33
1	9	101	356.062	396.634	145	1.37417	0.685884	13.5875	0.929487	0.74359	8423	58.0897	60	47	69
1	9	102	358.12	38.9816	217	2.28678	0.899318	16.6221	0.90795	0.645833	4595	21.1751	21	17	26
1	9	103	358.408	69.4079	76	1.22377	0.576432	9.83698	0.894118	0.690909	7205	94.8026	99	76	114
1	9	104	358.364	137.455	11	1.13876	0.478395	3.74241	0.785714	0.6875	210	19.0909	19	14	22
1	9	105	370.203	313.176	148	1.83856	0.839147	13.7273	0.89697	0.621849	4306	29.0946	30	22	35
1	9	106	373.012	202.524	166	2.28347	0.89901	14.5381	0.922222	0.65873	4596	27.6867	29	21	34
1	9	107	377.777	170.057	404	1.31694	0.650698	22.6801	0.930876	0.706294	20716	51.2772	52	38	64
1	9	108	384.198	243.899	328	1.6475	0.794718	20.4358	0.931818	0.788462	12022	36.6524	37	27	46
1	9	109	375.638	462.116	69	1.52244	0.75403	9.37302	0.896104	0.627273	3544	51.3623	52	41	62
1	9	110	383.181	491.839	155	1.6691	0.800655	14.0482	0.922619	0.645833	5726	36.9419	38	29	45
1	9	111	392.202	297.197	213	1.27925	0.623648	16.4682	0.926087	0.739583	6337	29.7512	30	22	38
1	9	112	391.713	407.231	195	1.80111	0.831707	15.757	0.924171	0.714286	9007	46.1897	48	35	58
1	9	113	404.037	455.366	82	1.57912	0.773937	10.2179	0.911111	0.759259	3945	48.1098	51	38	59
1	9	114	418.117	476.067	60	1.24455	0.595299	8.74039	0.869565	0.666667	4998	83.3	85	63	101
1	9	115	430.121	389.29	124	1.23756	0.589125	12.5651	0.905109	0.738095	4216	34	35	26	41
1	9	116	434.672	217.156	250	1.45536	0.72655	17.8412	0.93985	0.730994	9416	37.664	39	30	46
1	9	117	430.222	486.361	72	1.21482	0.567797	9.57461	0.878049	0.72	3740	51.9444	52	41	61
1	9	118	438.356	245.69	323	3.93418	0.967156	20.2795	0.813602	0.419481	11119	34.4241	36	27	42
1	9	119	444.212	361.171	316	2.27398	0.898116	20.0585	0.863388	0.548611	17939	56.769	58	43	71
1	9	120	441.239	288.096	230	1.75024	0.820706	17.1127	0.927419	0.684524	9461	41.1348	42	31	51
1	9	121	442.21	57.6643	143	1.34234	0.667097	13.4935	0.922581	0.744792	8260	57.7622	60	45	70
1	9	122	441.885	437.769	52	1.40181	0.700796	8.13686	0.896552	0.742857	3533	67.9423	70	53	81
1	9	123	450.907	139.683	161	2.22932	0.893749	14.3175	0.92	0.731818	4391	27.2733	27	20	35
1	9	124	453.118	424.193	119	1.29823	0.637708	12.3092	0.901515	0.708333	4146	34.8403	36	27	42
1	9	125	452.477	462.156	128	1.1575	0.503605	12.7662	0.920863	0.757396	4293	33.5391	35	26	40
1	9	126	455.773	440.5	44	1.23615	0.58786	7.48482	0.88	0.785714	3328	75.6364	77	62	90
1	9	127	474.277	407.954	130	1.41995	0.709952	12.8655	0.915493	0.714286	7021	54.0077	56	44	66
1	9	128	479.27	187.428	152	1.48858	0.740748	13.9116	0.853933	0.633333	4951	32.5724	33	26	40
1	9	129	479.157	215.248	121	1.27349	0.61919	12.4122	0.902985	0.715976	4343	35.8926	37	28	43
1	9	130	480.898	10.1837	49	1.4708	0.733302	7.89865	0.907407	0.777778	5891	120.224	122	92	147
1	9	131	485.018	132.565	168	1.6403	0.792675	14.6255	0.933333	0.777778	4290	25.5357	26	20	32
1	9	132	488.025	230.544	160	1.36575	0.68109	14.273	0.946746	0.784314	8081	50.5063	53	41	62
1	9	133	489.527	41.2545	165	1.47325	0.73435	14.4943	0.911602	0.705128	4206	25.4909	27	20	31
1	9	134	488.927	311.45	191	1.39613	0.697829	15.5945	0.927184	0.702206	9350	48.9529	50	38	60
1	9	135	493.91	94.3349	212	2.14811	0.885034	16.4294	0.921739	0.658385	7500	35.3774	38	29	41
1	9	136	495.135	339.708	192	1.32749	0.657674	15.6353	0.932039	0.761905	8831	45.9948	48	36	55
1	9	137	497.039	369.388	178	2.12112	0.881893	15.0545	0.92228	0.706349	6413	36.0281	38	27	44

APPENDIX B

Example of the summary output of AnalyseDNA.m program
(summary for 10 3 by 3 montage images)

1	1187 32.4103	163.912 14.334	79.3918 50.5906	1.59849 22.6584	0.398735	0.726461	0.137996	14.0612	3.315	0.905327	0.0350365	0.701248	0.075176	6449.26	3496.95	41.539	18.352	42.9444	18.9393
2	1305 33.0245	169.034 13.3362	86.8722 51.3609	1.60511 21.2507	0.399942	0.727835	0.138462	14.2634	3.43288	0.906571	0.0341453	0.70177	0.0730289	6786.37	3895.1	42.2416	17.0965	43.8245	17.583
3	1399 34.8313	164.57 16.2062	80.0679 54.4417	1.58728 25.1765	0.397935	0.72552	0.13163	14.0853	3.33904	0.905267	0.0361822	0.702891	0.0720005	6881.08	3525.81	44.7167	20.5918	46.3838	21.2287
4	1388 33.7349	172.075 15.9902	89.7145 52.505	1.60189 24.193	0.389682	0.727142	0.142518	14.3531	3.61812	0.902766	0.0374254	0.695945	0.0753889	6997.68	4212.87	43.1798	19.8582	44.9561	20.5112
5	1448 34.3315	171.921 16.6358	90.64 53.6367	1.58887 26.5398	0.400493	0.721084	0.141204	14.338	3.65065	0.904152	0.0379804	0.70023	0.0756884	7050.22	4163.04	44.0559	21.4761	45.8522	22.1282
6	1418 34.5444	165.142 15.2864	84.6806 53.9055	1.60542 23.8472	0.425512	0.728414	0.133721	14.0974	3.39686	0.904614	0.0362731	0.696204	0.0782855	6843.2	3924.12	44.266	19.3396	45.9485	19.8324
7	1756 26.8901	129.864 17.0421	99.2039 43.0689	1.57806 25.6082	0.451022	0.694813	0.185667	11.728	5.27441	0.893311	0.0481729	0.704526	0.0892393	5162.51	4393.11	34.9743	21.1969	36.16	22.0024
8	1280 33.0602	171.587 13.7194	84.1254 51.3961	1.59301 20.956	0.405467	0.723421	0.137599	14.3833	3.40593	0.906384	0.0357179	0.702574	0.0751602	6865.87	3767.48	42.2752	17.2223	43.9781	17.7621
9	1270 32.3669	166.53 13.8149	86.5094 50.6976	1.60367 22.2407	0.404986	0.72668	0.138548	14.1402	3.47794	0.905208	0.0356298	0.700331	0.0766773	6576.54	4022.38	41.6064	17.8994	43.163	18.2499
10	1425 34.4582	159.606 16.3199	83.618 53.7958	1.57286 25.6094	0.400372	0.717147	0.139085	13.8205	3.49536	0.904275	0.0379111	0.702759	0.07572	6587.18	3788.39	44.2141	20.7694	45.8765	21.136

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